

Access DB#

4/622

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: _____ Examiner #: _____ Date: _____
 Art Unit: _____ Phone Number 30 _____ Serial Number: _____
 Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

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Type of Search

Vendors and cost where applicable

Searcher: <u>D. Schreiber</u>	NA Sequence (#) _____	STN _____
Searcher Phone #: <u>308-4292</u>	AA Sequence (#) <u>1</u>	Dialog _____
Searcher Location: <u>CM1 12E18</u>	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up: _____	Bibliographic _____	Dr.Link _____
Date Completed: <u>5/4</u>	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time: <u>4</u>	Fulltext _____	Sequence Systems <u>Compugen</u>
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Online Time: <u>6</u>	Other _____	Other (specify) _____

41622

STIC-Biotech/ChemLib

From: Seharaseyon, Jegatheesan
Sent: Wednesday, May 02, 2001 3:59 PM
To: STIC-Biotech/ChemLib
Subject: Re:09/467160

Please search the commercial database for SEQ ID:3 of 09/467,160. Thanks.

J.Seharaseyon
Art Unit 1647
CM1 10D16
10CO1 MB
(703)-305-1112

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 4, 2001, 07:35:28 ; Search time 18.57 Seconds
(without alignments)
224.713 Million cell updates/sec

Title: US-09-467-160-3

Perfect score: 379

Sequence: 1 APLATELRCCQLTQIHL.....PASPMPVKRIIEKMLKNGKSN 73

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 390729 seqs, 57163235 residues

Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_0401.*

- 1: /SID56/gcgdata/geneseq/geneseq/AA1980.DAT.*
- 2: /SID56/gcgdata/geneseq/geneseq/AA1981.DAT.*
- 3: /SID56/gcgdata/geneseq/geneseq/AA1982.DAT.*
- 4: /SID56/gcgdata/geneseq/geneseq/AA1983.DAT.*
- 5: /SID56/gcgdata/geneseq/geneseq/AA1984.DAT.*
- 6: /SID56/gcgdata/geneseq/geneseq/AA1985.DAT.*
- 7: /SID56/gcgdata/geneseq/geneseq/AA1986.DAT.*
- 8: /SID56/gcgdata/geneseq/geneseq/AA1987.DAT.*
- 9: /SID56/gcgdata/geneseq/geneseq/AA1988.DAT.*
- 10: /SID56/gcgdata/geneseq/geneseq/AA1989.DAT.*
- 11: /SID56/gcgdata/geneseq/geneseq/AA1990.DAT.*
- 12: /SID56/gcgdata/geneseq/geneseq/AA1991.DAT.*
- 13: /SID56/gcgdata/geneseq/geneseq/AA1992.DAT.*
- 14: /SID56/gcgdata/geneseq/geneseq/AA1993.DAT.*
- 15: /SID56/gcgdata/geneseq/geneseq/AA1994.DAT.*
- 16: /SID56/gcgdata/geneseq/geneseq/AA1995.DAT.*
- 17: /SID56/gcgdata/geneseq/geneseq/AA1996.DAT.*
- 18: /SID56/gcgdata/geneseq/geneseq/AA1997.DAT.*
- 19: /SID56/gcgdata/geneseq/geneseq/AA1998.DAT.*
- 20: /SID56/gcgdata/geneseq/geneseq/AA1999.DAT.*
- 21: /SID56/gcgdata/geneseq/geneseq/AA2000.DAT.*
- 22: /SID56/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	379	100.0	73	14 R36771	MIP-2alpha. Homo
2	379	100.0	73	16 R66699	Human gro-beta che
3	379	100.0	73	18 W18025	Human chemokine gr
4	379	100.0	73	18 W17671	Human chemokine gr
5	379	100.0	73	20 Y18104	Human gro-beta pro
6	379	100.0	73	20 W81499	Human gro-beta pol
7	379	100.0	73	21 Y69036	Amino acid sequenc
8	379	100.0	107	13 R20589	Human macrophage i
9	379	100.0	107	13 R20529	Human macrophage i
10	379	100.0	107	13 R23034	Human Gro beta cyt
11	379	100.0	107	20 W96714	Growth related onc

12	379	100.0	107	21	B15810	Human chemokine GR
13	352	92.9	102	16	R70793	Gro-beta/MIP-2- α p
14	331	87.3	73	16	R66698	Human gro-alpha ch
15	331	87.3	73	18	W18024	Human chemokine gr
16	331	87.3	73	18	W17670	Human chemokine gr
17	331	87.3	73	20	Y18106	Human gro-alpha pr
18	331	87.3	73	20	W81498	Human mature gro-a
19	331	87.3	73	21	Y69026	Amino acid sequenc
20	331	87.3	107	20	W96713	Growth related onc
21	331	87.3	107	21	B15793	Human chemokine GR
22	331	87.3	107	21	B15813	Human chemokine GR
23	330	87.1	107	16	R70792	Melanoma growth st
24	325	85.8	73	14	R36772	MIP-2beta. Homo s
25	325	85.8	73	16	R66700	Human gro-gamma ch
26	325	85.8	73	17	R93194	Protein used to ge
27	325	85.8	73	18	W18026	Human chemokine gr
28	325	85.8	73	20	Y18107	Human gro-gamma pr
29	325	85.8	73	20	W81500	Human mature gro-g
30	325	85.8	73	21	Y69037	Amino acid sequenc
31	325	85.8	106	13	R23035	Human Gro gamma cy
32	325	85.8	106	20	W96715	Growth related onc
33	325	85.8	107	13	R20590	Human macrophage i
34	325	85.8	107	16	R70794	Gro-gamma/MIP-2-be
35	323	85.2	73	18	W17672	Human chemokine gr
36	318	83.9	107	13	R20530	Human macrophage i
37	284	74.9	72	12	R14077	Cytokine and neutr
38	283	74.7	73	18	W12434	Chimeric interleuk
39	278	73.4	72	16	R66697	Mouse KC chemokine
40	278	73.4	72	18	W18023	Murine chemokine K
41	278	73.4	72	18	W17669	Murine chemokine K
42	278	73.4	72	20	Y18105	Murine protein KC.
43	278	73.4	72	20	W81497	Mouse mature KC po
44	267.5	70.6	72	18	W12436	Chimeric interleuk
45	261	68.9	100	11	R05790	Macrophage derived

ALIGNMENTS

RESULT	1
R36771	ID R36771 standard; protein; 73 AA.
XX	AC R36771;
XX	DT 29-SEP-1993 (first entry)
XX	DE MIP-2alpha.
XX	Macrophage inflammatory protein; megakaryocytopoiesis; MIP-1; MIP-2;
KW	thrombocythemia; reactive thrombocytosis; stroke; emboli; platelet;
KW	myeloproliferative disorder.
XX	OS Homo sapiens.
XX	PN WO9309799-A.
XX	PD 27-MAY-1993.
XX	PF 13-NOV-1992; 92MO-US09671.
XX	PR 15-NOV-1991; 91US-0792988.
XX	(UYPE-) UNIV PENNSYLVANIA.
XX	Gewirtz AM;
XX	WPI; 1993-182239/22.
XX	Suppression of megakaryocytopoiesis - by administration of
XX	macrophage inflammatory protein-1 or -2
PS	Disclosure; Page 18; 26pp; English.

XX A claimed method for reducing the no. of circulating platelets in the
 CC bloodstream of a mammal comprises admin. of MIP-1 and/or MIP-2 or
 CC their analogues to induce such a reduction. The MIP-1, MIP-2 or
 CC analogue may be operatively linked to a carrier. The MIPs can be
 CC used to inhibit megakaryocytopoiesis to effect in vivo reduction of
 CC platelet nos. They can be used to treat disorders with excessively
 CC high platelet counts such as thrombocytosis, stroke, pulmonary emboli
 CC and myeloproliferative disorders.
 XX
 SQ Sequence 73 AA;

Query Match 100.0%; Score 379; DB 14; Length 73;
 Best Local Similarity 100.0%; Pred. No. 1.4e-38;
 Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APLATELCOCLOTLQGIHLKNIQSVKSPGPHCAQTEVIATLKNGQKACLNPA SPVVK 60
 DB 1 aplatelrcqlgtlqgihlknigsvkvspgphcaqteviatlknqgkaclnpasmvk 60
 DB 61 KIIEKMLKNGKSN 73
 61 kiiekmlkngksn 73

RESULT 2
 ID R66699 standard; protein; 73 AA.
 AC R66699;
 XX
 XX 19-JUL-1995 (first entry)
 DT Human gro-beta chemokine.
 XX
 KW Gro-alpha protein; chemokine; inflammation; antiinflammatory;
 KW hematopoietic synergistic factor; HSF; hematopoietic precursor;
 KW bone marrow; intercrine; desamino gro-beta; truncation.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Protein 5..73
 FT /note= "desamino truncated gro-beta, claim 6,
 FT page 68"
 XX
 PN WO9429341-A.
 XX
 XX 22-DEC-1994.
 PF 03-JUN-1994; 94WO-US06264.
 XX
 PR 08-JUN-1993; 93US-0073800.
 XX
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 PA Balcarek JM, Bhatnagar P, King AG, Pelus LM;
 PI WPI; 1995-036402/05.
 DR
 XX New truncated chemokine with increased biological activity - and
 XX related multimers, nucleic acid, antibodies etc., for treating
 PT inflammation, stimulating growth of bone marrow etc., also
 PT peptide(s) for inducing haematopoietic synergistic factor.
 XX
 XX Disclosure; Page 51-52; 89pp; English.
 PS
 XX Truncated, desamino chemokine comprising amino acids 5-73 of
 CC human mature gro-beta (full sequence given in R66699)
 CC shows enhanced biological activity when compared to the mature
 CC protein, and has been used to prepare multimeric, modified
 CC chemokines.

XX Sequence 73 AA;
 SQ

Query Match 100.0%; Score 379; DB 16; Length 73;
 Best Local Similarity 100.0%; Pred. No. 1.4e-38;
 Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APLATELCOCLOTLQGIHLKNIQSVKSPGPHCAQTEVIATLKNGQKACLNPA SPVVK 60
 DB 1 aplatelrcqlgtlqgihlknigsvkvspgphcaqteviatlknqgkaclnpasmvk 60
 QY 61 KIIEKMLKNGKSN 73
 DB 61 kiiekmlkngksn 73

RESULT 3
 ID W18025 standard; protein; 73 AA.
 AC W18025;
 XX
 XX 30-JAN-1998 (first entry)
 DT Human chemokine gro beta.
 XX
 DE Human chemokine gro beta.
 XX
 KW Sepsis; septic shock; therapy; gro beta; chemokine; human.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Protein 5..73
 FT /note= "preferred modified fragment of KC
 FT (Claim 2)"
 XX
 PN WO9719173-A1.
 XX
 XX 29-MAY-1997.
 PD
 XX 20-NOV-1996; 96WO-US18616.
 PF
 PR 21-NOV-1995; 95US-0007425.
 XX
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 PA
 XX DeMarsh PL, Johanson KO;
 PI WPI; 1997-298111/27.
 XX
 XX Use of chemokine(s) such as KC and gro-alpha - to treat or prevent
 PT sepsis, particularly septic shock
 PT
 PS Claim 1; Page 19; 28pp; English.
 XX
 XX A claimed method of treating or preventing sepsis comprises
 CC administering to an animal an effective amount of a chemokine
 CC selected from mature murine KC (see W18023), human gro alpha (see
 CC W18024), human gro beta (W18025) and human gro gamma (see
 CC W18026), modified fragments of these chemokines and multimeric
 CC proteins comprising an association of two chemokine proteins.
 CC Sepsis can occur in hospitalised patients, and a consequence of
 CC bacterial sepsis is septic shock. The method of the invention
 CC provides a treatment for sepsis, particularly septic shock, which
 CC is a major cause of death in intensive care units. Septic shock
 CC syndrome apparently has intractable resistance to the effects of
 CC a variety of highly potent antimicrobial agents. Survival is
 CC increased by treatment with the chemokines, both prophylactically
 CC and after infection.
 XX
 XX Sequence 73 AA;
 SQ


```

Db      61 kliekmlkngksn 73

RESULT      6
W81499
ID      W81499 standard; Protein; 73 AA.
XX
XX      W81499;
XX
XX      01-MAR-1999 (first entry)
XX
XX      human gro-beta polypeptide used to treat sepsis.
DE
XX      Gro-beta; chemokine; human; sepsis; septic shock; therapy.
KW
XX      Mus sp.
OS
XX
XX      Key      Location/Qualifiers
FH      Protein      5..73
FT      /note= "claimed fragment"
FT
XX
XX      WC9848828-A1.
XX
XX      05-NOV-1998.
PD
XX
XX      29-APR-1998;      98WO-US08742.
PR
XX
XX      29-APR-1997;      97US-0846966.
XX
XX      (SMIK ) SMITHKLINE BEECHAM CORP.
PA
XX      Demarsh PL,  Johanson KO;
XX
XX      WPI; 1999-024031/02.
XX
XX      Treating and preventing sepsis in animals - by using two modified
PT      gro b chemokines in conjunction with an anti-infective agent
PT
XX
XX      Example 1; Page 18; 26pp; English.
XX
XX      This is the amino acid sequence of the human chemokine gro-beta
CC      mature polypeptide. The invention relates to a method of
CC      preventing and treating sepsis using chemokines selected from
CC      mature or modified murine KC (see W81497), or human gro-alpha (see
CC      W81498), gro-beta or gro-gamma (see W81499). A claimed method uses
CC      a dimeric chemokine consisting of 2 covalently linked modified
CC      gro-beta proteins (amino acids 5-73 of the mature polypeptide)
CC      in which the proteins are linked by 2 intermolecular disulphide
CC      bonds between C5-C31 and C7-C47. Further claimed is administering
CC      the chemokine in conjunction with an anti-infective agent. The
CC      chemokines described in this invention are required to treat and
CC      prevent sepsis since antimicrobial agents alone have failed to
CC      abrogate septic mortality.
XX
XX      Sequence      73 AA;

Query Match      100.0%; Score 379; DB 20; Length 73;
Best Local Similarity 100.0%; Pred. No. 1.4e-38;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 APLATELRCCQLQTLQGIHLKNIQSVKSPGPHCAQTEVIATLKGOKACLNPA5PMVK 60
      |
      |
      |
Db      1 aplatelrcqclqlgllhlnkigsvkvspgphcaqteviatlknqgkaclnpaspmvk 60
      |
      |
      |
Qy      61 KIEEMLKNGKSN 73
      |
      |
      |
Db      61 kliekmlkngksn 73

RESULT      7
Y69036
ID      Y69036 standard; protein; 73 AA.

```


KW Cytokine; inflammatory response; MAD-2; cancer diagnosis;
 KW colonic epithelial tumour cell.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Peptide 1..35

FT /label= leader

FT /note= "putative"

FT 36..107

FT Protein

FT /label= Gro_beta

XX W09206196-A.

PN 16-APR-1992.

PD 24-SEP-1991; 91WO-US06936.

XX 28-SEP-1990; 90US-0590223.

PR (CETU) CETUS CORP.

XX (UYNC-) UNIV OF NORTH CAROLINA.

PA Haskill JS, Nitecki DE, Ralph P;

XX WPI; 1992-150882/18.

DR N-PSDB; Q24266.

XX Gro beta and Gro gamma inflammatory cytokine(s) - for use in

PT diagnosing colon cancer

XX Claim 12; Fig 1B; 46pp; English.

XX The cDNA clone coding for inflammatory cytokine Gro-beta was

CC isolated from a mezerin- and calcium ionophore-stimulated leukocyte

CC cDNA library. The amino acid sequence of Gro beta was deduced from

CC the nucleotide sequence. The level of Gro beta in inflammatory

CC response cells can be used as an indication of a test substance's

CC inflammatory activity and to diagnose colon cancer.

XX See also Q24267.

XX Sequence 107 AA;

SQ

Query Match 100.0%; Score 379; DB 13; Length 107;

Best Local Similarity 100.0%; Pred. No. 2.3e-38;

Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APLATELRQCLOTLOGIHLKNIQSVKSPGPHCAQTEVIATLKNGKACLNPAWPK 60

|||||

35 APLATELRQCLOTLOGIHLKNIQSVKSPGPHCAQTEVIATLKNGKACLNPAWPK 94

QY 61 KIEKMLKNGKSN 73

|||||

95 KIEKMLKNGKSN 107

Db

RESULT 11

W96714

ID W96714 standard; Protein; 107 AA.

XX AC W96714;

XX 15-APR-1999 (first entry)

DT Growth related oncogene-beta (GRO-beta).

XX Growth related oncogene-beta; GRO-beta; CXC chemokine; metastasis;

XX angiogenesis inhibitor; angiostasis inducer; tumour growth inhibition;

XX haemangiomas; rheumatoid arthritis; atherosclerosis; meningioma;

XX idiopathic pulmonary fibrosis; benign prostatic hypertrophy; psoriasis;

XX vascular restenosis; arteriovenous malformation; neovascular glaucoma;

XX angiofibroma; haemophilic joint; hypertrophic scar; Osler-Weber syndrome;

KW

KW

KW

KW

KW

XX

XX

OS

XX

PN

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PD

XX

PF

XX

PR

XX

PA

XX

PI

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DR

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PT

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PT

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PS

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pyogenic granuloma retrolental fibroplasia; scleroderma; trachoma;
 vascular adhesion; synovitis; dermatitis; endometriosis; pterygium;
 diabetic retinopathy; neovascularisation; chronic bronchitis;
 adult respiratory distress syndrome; ARDS; pseudogout;
 cystic fibrosis.

Homo sapiens.

US5871723-A.

16-FEB-1999.

06-JUN-1995; 95US-0468819.

06-JUN-1995; 95US-0468819.

(UNMI) UNIV MICHIGAN.

Kunkel SL, Polverini PJ, Strieter RM;

WPI; 1999-166569/14.

N-PSDB; X15002.

Use of chemokines with a conserved Cys Xaa Cys (CXC) sequence -

which do not contain amino acid sequence ELR, for inhibiting

angiogenesis in tumours, rheumatoid arthritis, restenosis or

glaucoma

Disclosure; Columns 95-96; 145pp; English.

The present sequence is a growth related oncogene-beta (GRO-beta).

GRO-alpha is a CXC chemokine that is an inhibitor of angiogenesis.

The specification describes methods for inhibiting angiogenesis or for

inducing angiostasis, using chemokines (with a conserved Cys Xaa Cys

(CXC) sequence at the N-terminal) other than platelet factor-4, and

which do not contain the amino acid sequence ELR. The methods are useful

for inhibiting tumour growth and metastasis and for treating diseases

such as haemangiomas, rheumatoid arthritis, atherosclerosis and

idiopathic pulmonary fibrosis (IPF), benign prostatic hypertrophy (BPH),

vascular restenosis, arteriovenous malformations (AVM), meningioma,

neovascular glaucoma, psoriasis, angiofibroma, haemophilic joints,

hypertrophic scars, Osler-Weber syndrome, pyogenic granuloma retrolental

fibroplasia, scleroderma, trachoma, vascular adhesions, synovitis,

dermatitis, endometriosis, pterygium, diabetic retinopathy

neovascularisation associated with corneal injury or grafts, adult

respiratory distress syndrome (ARDS), chronic bronchitis, pseudogout

and cystic fibrosis.

Sequence 107 AA;

Query Match 100.0%; Score 379; DB 20; Length 107;

Best Local Similarity 100.0%; Pred. No. 2.3e-38;

Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APLATELRQCLOTLOGIHLKNIQSVKSPGPHCAQTEVIATLKNGKACLNPAWPK 60

|||||

35 APLATELRQCLOTLOGIHLKNIQSVKSPGPHCAQTEVIATLKNGKACLNPAWPK 94

QY 61 KIEKMLKNGKSN 73

|||||

95 KIEKMLKNGKSN 107

Db

RESULT 12

B15810

ID B15810 standard; Protein; 107 AA.

XX AC B15810;

XX 17-JAN-2001 (first entry)

DT Human chemokine GRObeta SEQ ID NO: 53.

XX

XX Macrophage recruitment; chemokine derivative; MCP-1; osteoporosis;
 KW monocyte chemoattractant protein-1; inflammation; atherosclerosis; HIV;
 KW AIDS; stroke; psoriasis; autoimmune disease; hypertension; endotoxaemia;
 KW basophil-mediated disease; myocardial infarction; acute ischaemia;
 KW rheumatoid arthritis; contraception.

XX Homo sapiens.

XX WO200042071-A2.

XX 20-JUL-2000.

XX 12-JAN-2000; 2000WO-US00821.

XX 12-JAN-1999; 99US-0229071.

XX 17-MAR-1999; 99US-0271192.

XX 01-DEC-1999; 99US-0452406.

XX (NEOR-) NEORX CORP.

XX Grainger DJ, Tatalick LM;

XX WPI; 2000-499101/44.

XX DR N-PSDB; A74871.

XX New peptide 3, amide and heterocyclic compounds and saccharide
 PT conjugates used for inhibiting chemokine induced activity and for
 PT treating e.g. stroke, vascular diseases, autoimmune diseases and tumour
 PT growth -
 XX Disclosure; Page 364; 387pp; English.

XX The present invention concerns the identification of a number of
 CC chemokines which can be used to produce derivatives, agonists and
 CC antagonists which are then useful in disease treatment. The chemokines
 CC include sequences B15785-B15794, B15803-B15813 and B15831-B15848. These
 CC chemokine derivatives can be used to treat diseases such as autoimmune
 CC diseases, atherosclerosis, osteoporosis, HIV infection and AIDS,
 CC psoriasis, inflammatory diseases, hypertension, basophil-mediated
 CC diseases, endotoxaemia, myocardial infarction, acute ischaemia and
 CC rheumatoid arthritis, and can be used to prevent strokes and as
 CC contraceptives. The coding sequences for the chemokines can be used in
 CC gene therapy for the same diseases, as well as in the production of
 CC animal models.

XX Sequence 107 AA;

Query Match 100.0%; Score 379; DB 21; Length 107;
 Best Local Similarity 100.0%; Pred. No. 2.3e-38;
 Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APLATELRCQCLOTLQGIHLNIGSVKSPGPHCAQTEVIATLNGOKACLNPSPMVK 60

|||||
 Db 35 aplatelrcqltqlgihlnigsvkspgphcaqteviatlknqgkaclnpspmvk 94

QY 61 KIIEKMLKNGKSN 73

|||||
 Db 95 kiiekmlkngksn 107

RESULT 13

R70793

ID R70793 standard; Protein; 102 AA.

XX R70793;

XX 29-AUG-1995 (first entry)

XX Gro-beta/MIP-2-alpha.

XX Macrophage inflammatory protein 2-alpha; gro-beta/MIP-2-alpha;

KW heparanase; heparin; heparan sulfate; arthritis; restenosis;
 KW cancer; wound healing.

XX Homo sapiens.

XX WO9504158-A.

XX 09-FEB-1995.

XX 26-JUL-1994; 94WO-US08207.

XX 29-JUL-1993; 93US-0099866.

XX 13-OCT-1993; 93US-0136117.

XX (UPJO) UPJOHN CO.

XX Hoogwerf AJ, Ledbetter SR;

XX WPI; 1995-082239/11.

XX DR N-PSDB; Q85363.

XX Screening for cpds. with anti-heparanase activity - by detecting
 PT inhibition of heparin or heparan sulphate degradation,
 PT potentially useful for treating arthritis, restenosis, cancer.

XX Claim 12; Page 40; 60pp; English.

XX Purified heparanases, prepared under reducing conditions and
 CC activated with transglutaminase, are given in R70786-804. Most
 CC are prepared by reverse transcription of mRNA from activated human
 CC leukocytes, then cloning of the cDNA into pVL1392 baculovirus
 CC vector, and expression in Sf9 cells in the presence of reduced
 CC glutathione and dithiothreitol.

XX Sequence 102 AA;

Query Match 92.9%; Score 352; DB 16; Length 102;
 Best Local Similarity 100.0%; Pred. No. 3.9e-35;
 Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APLATELRCQCLOTLQGIHLNIGSVKSPGPHCAQTEVIATLNGOKACLNPSPMVK 60

|||||
 Db 35 aplatelrcqltqlgihlnigsvkspgphcaqteviatlknqgkaclnpspmvk 94

QY 61 KIIEKMLK 68

|||||
 Db 95 kiiekmlk 102

RESULT 14

R66698

ID R66698 standard; protein; 73 AA.

XX R66698;

XX 19-JUL-1995 (first entry)

XX Human gro-alpha chemokine..

XX Gro-alpha protein; chemokine; inflammation; antiinflammatory;
 KW hematopoietic synergistic factor; HSF; hematopoietic precursor;
 KW bone marrow; interleukin; desamino gro-alpha; truncation.

XX Homo sapiens.

XX Location/Qualifiers

XX Key 5..732

XX Protein

XX /note= "desamino truncated gro-alpha, claim 7,

XX page 69"

XX WO9429341-A.

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 4, 2001, 07:35:28 ; Search time 11.75 Seconds
(without alignments)
119.353 Million cell updates/sec

Title: US-09-467-160-3
Perfect score: 379
Sequence: 1 APLATELRCQQLTQGIHL.....PASPMVKIIEKMLKNGKSN 73

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 185757 seqs, 19210857 residues

Total number of hits satisfying chosen parameters: 185757

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	379	100.0	73	1	US-07-792-988-3
2	379	100.0	73	1	US-07-778-413E-19
3	379	100.0	73	1	US-08-340-102-19
4	379	100.0	73	2	US-08-436-420-27
5	379	100.0	73	3	US-08-846-966-3
6	379	100.0	73	3	US-08-557-142-3
7	379	100.0	73	5	PCT-US94-06264-3
8	379	100.0	107	1	US-08-352-324A-4
9	379	100.0	107	2	US-08-862-607-4
10	379	100.0	107	2	US-08-468-819-6
11	379	100.0	107	3	US-09-203-235-4
12	379	100.0	107	5	PCT-US95-16144-4
13	367	96.8	73	1	US-08-330-163-3
14	367	96.8	73	1	US-08-482-111-3
15	331	87.3	73	1	US-07-778-413E-18
16	331	87.3	73	1	US-08-340-102-18
17	331	87.3	73	1	US-08-330-163-2
18	331	87.3	73	1	US-08-482-111-2
19	331	87.3	73	2	US-08-436-420-26
20	331	87.3	73	3	US-08-846-966-2
21	331	87.3	73	3	US-08-557-142-2
22	331	87.3	73	5	PCT-US94-06264-2
23	331	87.3	107	1	US-08-352-324A-7
24	331	87.3	107	2	US-08-862-607-7
25	331	87.3	107	2	US-08-468-819-5
26	331	87.3	107	3	US-09-203-235-7
27	331	87.3	107	5	PCT-US95-16144-7

28	325	85.8	73	1	US-07-792-988-4	Sequence 4, Appli
29	325	85.8	73	1	US-07-778-413E-20	Sequence 20, Appl
30	325	85.8	73	1	US-08-340-102-20	Sequence 4, Appli
31	325	85.8	73	1	US-08-330-163-4	Sequence 4, Appli
32	325	85.8	73	1	US-08-482-111-4	Sequence 28, Appl
33	325	85.8	73	2	US-08-436-420-28	Sequence 4, Appli
34	325	85.8	73	3	US-08-846-966-4	Sequence 4, Appli
35	325	85.8	73	3	US-08-557-142-4	Sequence 4, Appli
36	325	85.8	73	5	PCT-US94-06264-4	Sequence 5, Appli
37	325	85.8	106	1	US-08-352-324A-5	Sequence 5, Appli
38	325	85.8	106	2	US-08-862-607-5	Sequence 5, Appli
39	325	85.8	106	2	US-08-468-819-7	Sequence 7, Appli
40	325	85.8	106	3	US-09-203-235-5	Sequence 5, Appli
41	325	85.8	106	5	PCT-US95-16144-5	Sequence 5, Appli
42	296	78.1	78	2	US-08-436-420-38	Sequence 38, Appl
43	284	74.9	72	2	US-08-436-420-39	Sequence 39, Appl
44	278	73.4	72	3	US-08-846-966-1	Sequence 1, Appli
45	278	73.4	72	3	US-08-557-142-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-07-792-988-3
; Sequence 3, Application US/07792988
; Patent No. 5306709
; GENERAL INFORMATION:
; APPLICANT: Gewirtz, Alan M.
; TITLE OF INVENTION: Suppression of megakaryo-
; TITLE OF INVENTION: cytopoiesis by macrophage inflammatory proteins
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: University of Pennsylvania
; STREET: Suite 419
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19104-3246
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07792,988
; FILING DATE: 19911115
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Monaco, Daniel A.
; REGISTRATION NUMBER: 30,480
; REFERENCE/DOCKET NUMBER: 6056-159
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-8383
; TELEFAX: (215) 568-5549
; TELEX: No. 5306709e
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 73 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single stranded
; TOPOLOGY: linear
US-07-792-988-3

Query Match 100.0%; Score 379; DB 1; Length 73;
Best Local Similarity 100.0%; Pred No. 1.7e-40;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 APLATELCOCLOTLOGIHLKNIQSVKSPGPHCAQTEVIATLKGOKACLNPAWPK 60
Db 1 APLATELCOCLOTLOGIHLKNIQSVKSPGPHCAQTEVIATLKGOKACLNPAWPK 60
OY 61 KIIEKMLKNGKSN 73
Db 61 KIIEKMLKNGKSN 73

RESULT 2
US-07-778-413E-19
; Sequence 19, Application US/07778413E
; Patent No. 5401651
; GENERAL INFORMATION:
; APPLICANT: Walz, Alfred
; TITLE OF INVENTION: No. 5401651el Neutrophil
; TITLE OF INVENTION: Activating Factors
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 in., DS, 2.0 MB
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh OS 7.0
; SOFTWARE: Microsoft Word Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07778,413E
; FILING DATE: 16-OCT-1991
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Cook, Robert R.
; REGISTRATION NUMBER: 31602
; REFERENCE/DOCKET NUMBER: A-204
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (805) 499-8011
; TELEFAX: (805) 499-5725 EXTENSION 4955
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 73 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-778-413E-19

Query Match 100.0%; Score 379; DB 1; Length 73;
Best Local Similarity 100.0%; Pred. No. 1.7e-40;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 APLATELCOCLOTLOGIHLKNIQSVKSPGPHCAQTEVIATLKGOKACLNPAWPK 60
Db 1 APLATELCOCLOTLOGIHLKNIQSVKSPGPHCAQTEVIATLKGOKACLNPAWPK 60
OY 61 KIIEKMLKNGKSN 73
Db 61 KIIEKMLKNGKSN 73

RESULT 3
US-08-340-102-19
; Sequence 19, Application US/08340102
; Patent No. 5591718
; GENERAL INFORMATION:
; APPLICANT: Walz, Alfred
; TITLE OF INVENTION: No. 5591718el Neutrophil
; TITLE OF INVENTION: Activating Factors
; NUMBER OF SEQUENCES: 22
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; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 in., DS, 1.4 MB
; COMPUTER: MS-DOS
; OPERATING SYSTEM: MS-DOS 6.22
; SOFTWARE: Microsoft Word Version 5.1a for
; SOFTWARE: Macintosh
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/340,102
; FILING DATE: 15-NOV-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Cook, Robert R.
; REGISTRATION NUMBER: 31602
; REFERENCE/DOCKET NUMBER: A-204A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (805) 499-5725 EXTENSION 4955
; TELEFAX: (805) 499-8011
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 73 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-340-102-19

Query Match 100.0%; Score 379; DB 1; Length 73;
Best Local Similarity 100.0%; Pred. No. 1.7e-40;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 APLATELCOCLOTLOGIHLKNIQSVKSPGPHCAQTEVIATLKGOKACLNPAWPK 60
Db 1 APLATELCOCLOTLOGIHLKNIQSVKSPGPHCAQTEVIATLKGOKACLNPAWPK 60
OY 61 KIIEKMLKNGKSN 73
Db 61 KIIEKMLKNGKSN 73

RESULT 4
US-08-436-420-27
; Sequence 27, Application US/08436420
; Patent No. 5840524
; GENERAL INFORMATION:
; APPLICANT: VAN DAMME, Jo; and
; APPLICANT: PROOST, Paul
; TITLE OF INVENTION: GRANULOCYTE CHEMOTACTIC PROTEIN
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HALE and DORR LLP
; STREET: 1455 PENNSYLVANIA AVENUE, N.W.
; CITY: WASHINGTON
; STATE: DISTRICT OF COLUMBIA
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,420
; FILING DATE: 24-MAY-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
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APPLICATION NUMBER: PCT/EP93/03330
FILING DATE: 26-NOV-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/982,539
FILING DATE: 27-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: BAKER, Hollie L.
REGISTRATION NUMBER: 31,321
REFERENCE/DOCKET NUMBER: 102378.215
TELEPHONE: (202) 942-8400
TELEFAX: (202) 942-8484
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 73 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-436-420-27

Query Match 100.0%; Score 379; DB 2; Length 73;
Best Local Similarity 100.0%; Pred. No. 1.7e-40;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APLATELCQCLOTLQGIHLKNIQSVKSPGPHCAQTEVIATLKGOKACLNPA SPVK 60
Db 1 APLATELCQCLOTLQGIHLKNIQSVKSPGPHCAQTEVIATLKGOKACLNPA SPVK 60
QY 61 KIIEKMLKNGKSN 73
Db 61 KIIEKMLKNGKSN 73

RESULT 5
US-08-846-966-3
Sequence 3, Application US/08846966
Patent No. 6042821
GENERAL INFORMATION:
APPLICANT: SmithKline Beecham Corporation
APPLICANT: DeMarsh, Peter L.
APPLICANT: Johanson, Kyung O.
TITLE OF INVENTION: Method of Treating Sepsis
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation - Corporate Patents
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/846,966
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/007,425
FILING DATE: 21-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hall, Linda E.
REGISTRATION NUMBER: 31,763
REFERENCE/DOCKET NUMBER: P50417-1
TELEPHONE: 610-270-5016
TELEFAX: 610-270-5090
INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
LENGTH: 73 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-846-966-3

Query Match 100.0%; Score 379; DB 3; Length 73;
Best Local Similarity 100.0%; Pred. No. 1.7e-40;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APLATELCQCLOTLQGIHLKNIQSVKSPGPHCAQTEVIATLKGOKACLNPA SPVK 60
Db 1 APLATELCQCLOTLQGIHLKNIQSVKSPGPHCAQTEVIATLKGOKACLNPA SPVK 60
QY 61 KIIEKMLKNGKSN 73
Db 61 KIIEKMLKNGKSN 73

RESULT 6
US-08-557-142-3
Sequence 3, Application US/08557142
Patent No. 6080398
GENERAL INFORMATION:
APPLICANT: Pelus, Louis M
APPLICANT: Bhatnagar, Pradip K
APPLICANT: King, Andrew G
APPLICANT: Balcarek, Joanna M
TITLE OF INVENTION: Methods of Enhancing Bioactivity of
TITLE OF INVENTION: Chemokines
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation -
ADDRESSEE: Corporate Patents
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/557,142
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/073,800
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Hall, Linda E.
REGISTRATION NUMBER: 31,763
REFERENCE/DOCKET NUMBER: SBCEP50161
TELEPHONE: 215-270-5015
TELEFAX: 215-270-5090
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 73 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-557-142-3

Query Match 100.0%; Score 379; DB 3; Length 73;
Best Local Similarity 100.0%; Pred. No. 1.7e-40;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 8
US-08-352-324A-4
; Sequence 4, Application US/08352324A
; Patent No. 563149
; GENERAL INFORMATION:
; APPLICANT: Guegler, Karl J.

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RESULT          9
US-08-862-607-4
; Sequence 4, Application 05/08862607
; Patent No. 5844084
; GENERAL INFORMATION:
; APPLICANT: Guegler, Karl J.
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Wilde, Craig G.
; APPLICANT: Sellhammer, Jeffrey J.
; TITLE OF INVENTION: A NOVEL CHEMOKINE EXPRESSED IN
; TITLE OF INVENTION: INFLAMED ADENOID, ITS PRODUCTION AND USES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette

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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/862,607
FILING DATE: 23-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/352,324
FILING DATE: 07-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Luther, Barbara J.
REGISTRATION NUMBER: 33,954
REFERENCE/DOCKET NUMBER: PF-0025 US
TELEPHONE: 415-855-0555
TELEFAX: 415-852-0195
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-862-607-4

Query Match 100.0%; Score 379; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. NO. 2.7e-40;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APLATELRCCLOTLQGIHLKNIQSVKSPGPHCAQTEVIATLKGOKACLNPA5PMVK 60
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DB 35 APLATELRCCLOTLQGIHLKNIQSVKSPGPHCAQTEVIATLKGOKACLNPA5PMVK 94
|||||

QY 61 KIIEKMLKNGKSN 73
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DB 95 KIIEKMLKNGKSN 107
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RESULT 10
US-08-468-819-6
Sequence 6, Application US/08468819
Patent No. 5871723
GENERAL INFORMATION:
APPLICANT: Strieter, Robert M.
APPLICANT: Polverini, Peter J.
APPLICANT: Kunkel, Steven L.
TITLE OF INVENTION: CXK Chemokines as Regulators of
TITLE OF INVENTION: Angiogenesis
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: US
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,819
FILING DATE: Concurrently herewith
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: UMIC:003/HYL
TELEPHONE: 512/418-3000

TELEFAX: 512/474-7477
TELEX: N/A
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-468-819-6

Query Match 100.0%; Score 379; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. NO. 2.7e-40;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APLATELRCCLOTLQGIHLKNIQSVKSPGPHCAQTEVIATLKGOKACLNPA5PMVK 60
|||||
DB 35 APLATELRCCLOTLQGIHLKNIQSVKSPGPHCAQTEVIATLKGOKACLNPA5PMVK 94
|||||

QY 61 KIIEKMLKNGKSN 73
|||||
DB 95 KIIEKMLKNGKSN 107
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RESULT 11
US-09-203-235-4
Sequence 4, Application US/09203235
Patent No. 6071701
GENERAL INFORMATION:
APPLICANT: Guegler, Karl J.
APPLICANT: Hawkins, Phillip R.
APPLICANT: Wilde, Craig G.
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: A NOVEL CHEMOKINE EXPRESSED IN
TITLE OF INVENTION: INFLAMED ADENOID, ITS PRODUCTION AND USES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: US
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/203,235
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/862,607
FILING DATE: 23-MAY-1997
APPLICATION NUMBER: 08/352,324
FILING DATE: 07-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Luther, Barbara J.
REGISTRATION NUMBER: 33,954
REFERENCE/DOCKET NUMBER: PF-0025 US
TELEPHONE: 415-855-0555
TELEFAX: 415-852-0195
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-203-235-4


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US-08-330-163-3
; Sequence 3, Application US/08330163
; Patent No. 5656724
; GENERAL INFORMATION:
; APPLICANT: Daly, Thomas J.
; APPLICANT: LaRosa, Gregory J.
; TITLE OF INVENTION: Chemokine-Like Proteins and Methods of
; TITLE OF INVENTION: Use
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #I.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/330,163
; FILING DATE: 05-AUG-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Fasse, J. Peter
; REGISTRATION NUMBER: 32,983
; REFERENCE/DOCKET NUMBER: 00231/080001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 73 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-330-163-3

Query Match          96.8%; Score 367; DB 1; Length 73;
Best Local Similarity 97.3%; Pred. No. 5.4e-39;
Matches 71; Conservative 0; Mismatches 2; Indels 0; Gaps 0

Oy   1 APLATELCQCCLQTLOGTHLKNIOGVKVSFGPHCAQTEVIATLKNGOKACLNPASPMK 60
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Db    1 APLATELCQCCLQTLOGTHLKNIOGVNFKVSGPHCAQTEVIATLKNGOKACLNPASPMK 60
      |||||||

Oy   61 KIIEKMLKNGKSN 73
      |||||
Db    61 KIIEKMEKNGKSN 73
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RESULT 14
US-08-482-111-3
; Sequence 3, Application US/08482111
; Patent No. 5789539
; GENERAL INFORMATION:
; APPLICANT: Daly, Thomas J.
; APPLICANT: LaRosa, Gregory J.
; TITLE OF INVENTION: Chemokine-Like Proteins and Methods of
; TITLE OF INVENTION: Use
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:

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MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30B
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/482,111
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Fasse, J. Peter
 REGISTRATION NUMBER: 32,983
 REFERENCE/DOCKET NUMBER: 00231/083001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 542-5070
 TELEFAX: (617) 542-8906
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 73 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-482-111-3

Query Match 96.8%; Score 367; DB 1; Length 73;
 Best Local Similarity 97.3%; Pred. No. 5.4e-39;
 Matches 71; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 APLATELCQCCLQTQLOGIHLKNIQSVKSPGPHCAQTEVIATLKNQKACLNPA SPVK 60
 Db 1 APLATELCQCCLQTQLOGIHLKNIQSVKSPGPHCAQTEVIATLKNQKACLNPA SPVK 60

QY 61 KIIEKMLNKGKSN 73
 Db 61 KIIEKMLNKGKSN 73

RESULT 15
 US-07-778-413E-18
 Sequence 18, Application US/07778413E
 Patent No. 5401651
 GENERAL INFORMATION:
 APPLICANT: Walz, Alfred
 TITLE OF INVENTION: No. 5401651el Neutrophil
 TITLE OF INVENTION: Activating Factors
 NUMBER OF SEQUENCES: 22
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Amgen Inc.
 STREET: Amgen Center
 STREET: 1840 Dehavilland Drive
 CITY: Thousand Oaks
 STATE: California
 COUNTRY: USA
 ZIP: 91320-1789
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 in., DS, 2.0 MB
 COMPUTER: Apple Macintosh
 OPERATING SYSTEM: Macintosh OS 7.0
 SOFTWARE: Microsoft Word Version 5.1a
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/778,413E
 FILING DATE: 16-OCT-1991
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: Cook, Robert R.
 REGISTRATION NUMBER: 31602
 REFERENCE/DOCKET NUMBER: A-204
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (805) 499-5725 EXTENSION 4955
 TELEFAX: (805) 499-8011
 INFORMATION FOR SEQ ID NO: 18:
 SEQUENCE CHARACTERISTICS:

LENGTH: 73 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-07-778-413E-18

Query Match 87.3%; Score 331; DB 1; Length 73;
 Best Local Similarity 87.7%; Pred. No. 1.7e-34;
 Matches 64; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 APLATELCQCCLQTQLOGIHLKNIQSVKSPGPHCAQTEVIATLKNQKACLNPA SPVK 60
 Db 1 ASVATELCQCCLQTQLOGIHPKNIQSVKSPGPHCAQTEVIATLKNQKACLNPA SPVK 60

QY 61 KIIEKMLNKGKSN 73
 Db 61 KIIEKMLNKGKSN 73

Search completed: May 4, 2001, 07:36:40
 Job time: 72 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 4, 2001, 07:35:28 ; Search time 14.16 seconds
(without alignments)
354.292 Million cell updates/sec

Title: US-09-467-160-3
Perfect score: 379
Sequence: 1 APLATELRCCLOTLQIHL.....PASPMVKIIETKLNKNGSN 73

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

198801 seqs, 68722935 residues

Total number of hits satisfying chosen parameters: 198801

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_67.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	379	100.0	107	JH0281	macrophage inflamm
2	331	87.3	107	A28414	melanoma growth-st
3	325	85.8	107	B38290	GRO-gamma precurs
4	304	80.2	101	B28414	growth-regulated p
5	284	74.9	96	JN0572	neutrophil chemo-a
6	278	73.4	96	A32954	gro-alpha precurs
7	261	68.9	100	JH0200	macrophage inflamm
8	249	65.7	100	S21467	macrophage inflamm
9	249	65.7	100	I55614	macrophage inflamm
10	233	61.5	100	S46198	cytokine-induced n
11	212	55.9	53	I64831	gene KC protein -
12	210	55.4	117	B42531	macrophage inflamm
13	210	55.4	119	S24881	platelet basic pro
14	209	55.1	128	1 TGHU	beta-thromboglobul
15	208	54.9	75	B54188	granulocyte chemot
16	199.5	52.6	114	A55010	neutrophil-activat
17	178	47.0	53	I31886	macrophage inflamm
18	176.5	46.6	103	A26736	transformation-ind
19	176.5	46.6	103	I50417	RSV-induced protei
20	173	45.6	75	A54188	granulocyte chemot
21	173	45.6	90	S69133	platelet factor 4
22	168	44.3	125	JN0470	interferon gamma-i
23	166.5	43.9	105	A26774	platelet factor 4
24	166	43.8	36	S17507	cytokine - rabbit
25	164.5	43.4	99	A37034	interleukin-8 prec
26	163	43.0	132	A57325	C-X-C chemokine LI
27	160	42.2	101	1 PFH04	platelet factor 4
28	160	42.2	126	A35766	platelet factor 4
29	155.5	41.0	101	2 S42496	interleukin 8 - sh

30 155.5 41.0 101 2 146997 interleukin-8 - sh
31 151 39.8 33 2 S50035 cytokine boGRO - b
32 151 39.8 88 1 PF004 platelet factor 4
33 150.5 39.7 101 2 146871 interleukin-8 - ra
34 146.5 38.7 103 2 A44253 alveolar macrophag
35 146.5 38.7 103 2 A53096 interleukin-8 prec
36 145.5 38.4 95 2 JN0841 interleukin-8 - do
37 142 37.5 104 1 PFH04A platelet factor 4
38 130.5 34.4 101 2 148148 Neutrophil attract
39 113 29.8 98 1 TGHUGI interferon gamma-i
40 107 28.2 40 2 S33290 lipopolysaccharide
41 105 27.7 98 2 A45492 IP-10 precursor -
42 105 27.7 98 2 I59277 Mob-1 - rat
43 87.5 23.1 99 2 JG0182 chemokine BRAK - h
44 81.5 21.5 89 2 A53497 pre-B-cell growth-
45 81.5 21.5 89 2 I53416 interleukin-8 homo

ALIGNMENTS

RESULT 1

JH0281
macrophage inflammatory protein 2 alpha precursor - human
N;Alternate names: gro-beta; growth regulated protein beta; melanoma growth-stimulat
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 20-Aug-1999
C;Accession: JH0281; A35931; A38290; A60407
R;Tekamp-Olson, P.; Gallegos, C.; Bauer, D.; McClain, J.; Sherry, B.; Fabre, M.; van
J. Exp. Med. 172, 911-919, 1990
A;Title: Cloning and characterization of cDNAs for murine macrophage inflammatory pro
A;Reference number: JH0200; MUID:90354792
A;Accession: JH0281
A;Molecule type: mRNA
A;Residues: 1-107 <FEK>
A;Cross-references: GB:X53799; NID:g34658; PIDN:CAA37808.1; PID:g34659
R;Tida, N.; Grotendorst, G.R.
Mol. Cell. Biol. 10, 5596-5599, 1990
A;Title: Cloning and sequencing of a new gro transcript from activated human monocyte
A;Reference number: A35931; MUID:90377259
A;Accession: A35931
A;Molecule type: mRNA
A;Residues: 1-107 <IID>
A;Cross-references: GB:M57731; GB:M36964; NID:g183626; PIDN:AAA63182.1; PID:g183627
R;Haskill, S.; Peace, A.; Morris, J.; Sporn, S.A.; Anisowicz, A.; Lee, S.W.; Smith, T
Proc. Natl. Acad. Sci. U.S.A. 87, 7732-7736, 1990
A;Title: Identification of three related human GRO genes encoding cytokine functions.
A;Reference number: A38290; MUID:91017578
A;Accession: A38290
A;Molecule type: mRNA
A;Residues: 1-107 <HAS>
A;Cross-references: GB:M36820; NID:g183628; PIDN:AAA63183.1; PID:g183629
R;Sporn, S.A.; Elerman, D.F.; Johnson, C.E.; Morris, J.; Martin, G.; Ladner, M.; Hask
J. Immunol. 144, 4434-4441, 1990
A;Title: Monocyte adherence results in selective induction of novel genes sharing hom
A;Reference number: A60407; MUID:90257367
A;Accession: A60407
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 56-107 <SPO>
C;Superfamily: beta-thromboglobulin
C;Keywords: inflammation
F;1-34/Domain: signal sequence #status predicted <SIG>
F;35-107/Product: macrophage inflammatory protein 2 alpha #status predicted <MAT>

Query Match 100.0%; Score 379; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.3e-35;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APLATELRCCLOTLQIHLKNIQSVKSPGPHCAOTEVIATLNKOKACLNAPSPMKV 60
DB 35 APLATELRCCLOTLQIHLKNIQSVKSPGPHCAOTEVIATLNKOKACLNAPSPMKV 94

C; Superfamily: beta-thromboglobulin
F; 1-34/Domain: signal sequence #status predicted <STG>
F; 35-107/Product: melanoma growth-stimulatory activity

C:Species: Cricetulus griseus (Chinese hamster)
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 20-Aug-1999
C:Accession: B28414
R:Anisowicz, A.; Bardwell, L.; Sager, R.
Proc. Natl. Acad. Sci. U.S.A. 84, 7188-7192, 1987
A:Title: Constitutive overexpression of a growth-regulated gene in transformed Chinese hamster ovary cells
A:Reference number: A94184; MUID:86041072
A:Accession: B28414
A:Molecule type: mRNA
A:Residues: 1-101 <ANI>
A:Cross-references: GB:J03560; NID:g191088; PIDN:AAA36985.1; PID:g304509
A:Note: the authors translated the codon CAG for residue 52 as Glu
C:Superfamily: beta-thromboglobulin
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-101/Product: growth-regulated protein #status predicted <MAT>

Query Match 80.2%; Score 304; DB 2; Length 101;
Best Local Similarity 77.1%; Pred. No. 3.3e-27;
Matches 54; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 1 APLATELRCCQLOTLOGIHLKNIQSVKSPGPHCAQTEVIATLKNQKACLNPAASPVMVK 60
||| |||||||||: |:|||||||: || |||| |||||||||: |||||: |||:
Db 29 APVANELRCQCLQTMGVHLKNIQSLKVTPEPGHCTQTEVIATLKNQKACLNPEAPVMVQ 88
QY 61 KIIEKMLKNG 70
|||:|||||:
Db 89 KIVQKMLKSG 98
|||:|||||:
RESULT 5
JN0572
neutrophil chemo-attractant Gro protein precursor - rat
N:Alternate names: CINC; cytokine-induced neutrophil chemoattractant; interleukin-8-like
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 20-Jun-2000
C:Accession: JN0572; JQ1519; A34481; A48988; S51214
R:Konishi, K.; Takata, Y.; Yamamoto, M.; Yomogida, K.; Watanabe, K.; Tsurufuji, S.; Fujii
Gene 126, 285-286, 1993
A:Title: Structure of the gene encoding rat neutrophil chemo-attractant Gro.
A:Reference number: JN0572; MUID:93246259
A:Accession: JN0572
A:Molecule type: DNA
A:Residues: 1-96 <KON>
A:Cross-references: DDBJ:D11445; NID:g391854; PIDN:BAA02009.1; PID:g220755
Huang, S.; Paulauskis, J.D.; Kobzik, L.
J. Biochem. Biophys. Res. Commun. 184, 922-929, 1992
A:Title: Rat KC cDNA cloning and mRNA expression in lung macrophages and fibroblasts.
A:Reference number: JQ1519; MUID:92246987
A:Accession: JQ1519
A:Molecule type: mRNA
A:Residues: 1-32, 'S', 34-96 <HUA>
A:Cross-references: GB:M86536
A:Experimental source: alveolar macrophage
A:Note: the authors translated the codon AGT for residue 33 as Cys, AAC for residue 46 as
R:Watanabe, K.; Konishi, K.; Fujikoka, M.; Kinoshita, S.; Nakagawa, H.
J. Biol. Chem. 264, 19559-19563, 1989
A:Title: The neutrophil chemoattractant produced by the rat kidney epithelioid cell line
A:Reference number: A34481; MUID:90062049
A:Accession: A34481
A:Molecule type: protein
A:Residues: 25-96 <WAT>
R:Nakagawa, H.; Ikesue, A.; Hatakeyama, S.; Kato, H.; Gotoda, T.; Komorita, N.; Watanabe
Biochem. Pharmacol. 45, 1425-1430, 1993
A:Title: Production of an interleukin-8-like chemokine by cytokine-stimulated rat NRK-49
A:Reference number: A48988; MUID:93228656
A:Accession: A48988
A:Status: preliminary
A:Molecule type: protein
A:Residues: 25-57 <NAK>
A:Experimental source: kidney, NRK-49F fibroblasts
A:Note: sequence extracted from NCBI backbone (NCBIP:129132)
A:Accession: B48988

A:Status: preliminary
A:Molecule type: protein
A:Residues: 25-57 <NA2>
A:Experimental source: kidney, NRK-49F fibroblasts
A:Note: sequence extracted from NCBI backbone (NCBIP:129131)
R:Hanzawa, H.; Haryuyama, H.; Watanabe, K.; Tsurufuji, S.
FEBS Lett. 354, 207-212, 1994
A:Title: The three dimensional structure of rat cytokine CINC/Gro in solution by homo
A:Reference number: S51214; MUID:95046335
A:Contents: annotation; conformation by (1)H-NMR, residues 25-96
A:Accession: S51214
A:Molecule type: protein
A:Residues: 25-96 <HAN>
C:Comment: This protein has chemotactic activity for neutrophils and has melanoma gro
C:Genetics:
A:Gene: gro; KC
A:Introns: 24/1; 65/2; 92/2
C:Superfamily: beta-thromboglobulin
C:Keywords: cytokine; disulfide bond
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-96/Product: neutrophil chemo-attractant gro protein #status experimental <CYT>

Query Match 74.9%; Score 284; DB 2; Length 96;
Best Local Similarity 75.0%; Pred. No. 5.4e-25;
Matches 51; Conservative 10; Mismatches 7; Indels 0; Gaps 0;

QY 1 APLATELRCCQLOTLOGIHLKNIQSVKSPGPHCAQTEVIATLKNQKACLNPAASPVMVK 60
||| |||||||||: ||| |||||: || |||| |||||||||: |||||: |||:
Db 25 APVANELRCQCLQTVAGIHLKNIQSLKVPPEPGHCTQTEVIATLKNQKACLNPEAPVMVQ 84
QY 61 KIIEKMLK 68
|||:|||||:
Db 85 KIVQKMLK 92
|||:|||||:
RESULT 6
A32954
gro-alpha precursor - mouse
N:Alternate names: gro protein; growth regulated protein; melanoma growth-stimulating
C:Species: Mus musculus (house mouse)
C:Date: 20-Oct-1989 #sequence_revision 20-Oct-1989 #text_change 20-Aug-1999
C:Accession: A32954; JH0081
R:Oquendo, P.; Alberta, J.; Wen, D.; Graycar, J.L.; Derynck, R.; Stiles, C.D.
J. Biol. Chem. 264, 4133-4137, 1989
A:Title: The platelet-derived growth factor-inducible KC gene encodes a secretory pro
A:Reference number: A32954; MUID:89139485
A:Accession: A32954
A:Molecule type: mRNA
A:Residues: 1-96 <OQU>
A:Cross-references: GB:J04596; NID:g201042; PIDN:AAA40131.1; PID:g201043
R:Ryseck, R.P.; MacDonald-Bravo, H.; Mattei, M.G.; Bravo, R.
Exp. Cell Res. 180, 266-275, 1989
A:Title: Cloning and sequence of a secretory protein induced by growth factors in mou
A:Reference number: JH0081; MUID:89078302
A:Accession: JH0081
A:Molecule type: mRNA
A:Residues: 1-96 <RYS>
C:Comment: This protein is basic and lacks threonine, phenylalanine, and tyrosine.
A:Map position: 5
C:Superfamily: beta-thromboglobulin
C:Keywords: extracellular protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-96/Product: gro-alpha #status predicted <WAT>

Query Match 73.4%; Score 278; DB 2; Length 96;
Best Local Similarity 73.5%; Pred. No. 2.6e-24;
Matches 50; Conservative 11; Mismatches 7; Indels 0; Gaps 0;

QY 1 APLATELRCCQLOTLOGIHLKNIQSVKSPGPHCAQTEVIATLKNQKACLNPAASPVMVK 60
||| |||||||||: ||||| |||||: || |||| |||||||||: |||||: |||:

Query Match 61.5%; Score 233; DB 2; Length 100;
Best Local Similarity 62.7%; Pred. No. 3e-19;
Matches 42; Conservative 13; Mismatches 12; Indels 0; Gaps 0;

Qy 3 LATELRCCLOTLOGIHLKNIQSVKSPGPHCAQTEVIATLKNQKACLNPAASPMPVKKI 62
: | |||||: | : ||||| | ||||| |||||: ||| : | : ||
Db 31 VARELRCCLTPLRPVDENIQSLTVTPPGHCTQTEVIATLKDGOEVLNPOAPRLQKI 90
: | |||||: | : ||||| | ||||| |||||: ||| : | : ||

Qy 63 IEKMLKN 69
: | : ||| :

Db 91 IOKLKS 97
: | : ||| :

RESULT 11

I64831

Gene KC protein - rat (fragment)

C:Species: Rattus sp. (rat)

C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 23-Feb-1997

C:Accession: I64831

R: Huang, S.; Paulauskis, J.D.; Godleski, J.J.; Kobzik, L.

Am. J. Pathol. 141, 981-988, 1992

A:Title: Expression of macrophage inflammatory protein-2 and KC mRNA in pulmonary inflammation

A:Reference number: I51886; MUID:93035653

A:Accession: I64831

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-53 <RES>

A:Cross-references: GB:S45856; NID:g257055

C:Genetics:

A:Gene: KC

C:Superfamily: beta-thromboglobulin

Query Match 55.9%; Score 212; DB 2; Length 53;

Best Local Similarity 71.7%; Pred. No. 3.5e-17;

Matches 38; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

Qy 12 LQTLQGIHLKNIQSVKSPGPHCAQTEVIATLKNQKACLNPAASPMPVKKIE 64
: | |||||: | : ||||| | ||||| |||||: ||| : | : ||

Db 1 LQTVAGIHFKNIQSLKVMPPGPHCTQTEVIATLKNQKACLNPAASPMPVKIQV 53
: | |||||: | : ||||| | ||||| |||||: ||| : | : ||

RESULT 12

I44253

Alveolar macrophage chemotactic factor-II (AMCF-II) intercrine-alpha protein - pig

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 20-Aug-1999

C:Accession: B44253

R: Goodman, R.B.; Foster, D.C.; Mathewes, S.L.; Osborn, S.G.; Kuijper, J.L.; Forstrom, J.

Biochemistry 31, 10483-10490, 1992

A:Title: Molecular cloning of porcine alveolar macrophage-derived neutrophil chemotactic

A:Reference number: A44253; MUID:93041741

A:Accession: B44253

A:Status: preliminary

A:Molecule type: mRNA; protein

A:Residues: 1-117 <GO>

A:Cross-references: NID:g164325; PIDN:AAA30991.1; PID:g164326

A:Experimental source: alveolar macrophage

A:Note: sequence extracted from NCBI backbone (NCBIN:117417, NCBIPI:117418)

C:Superfamily: beta-thromboglobulin

Query Match 55.4%; Score 210; DB 2; Length 117;

Best Local Similarity 53.5%; Pred. No. 1.4e-16;

Matches 38; Conservative 14; Mismatches 19; Indels 0; Gaps 0;

Qy 1 APLATELRCCLOTLOGIHLKNIQSVKSPGPHCAQTEVIATLKNQKACLNPAASPMPVK 60
: | |||||: | : ||||| | ||||| |||||: ||| : | : ||

Db 44 AAVVRELRCNCLTTPGHPKMSIDLVIPAGPQCSKAEVIATLKNQKACLNPAASPMPVK 103
: | |||||: | : ||||| | ||||| |||||: ||| : | : ||

Qy 61 KIIEKMLKNGK 71
: | : ||| :

Db 104 KIVQKMLDSGK 114
: | : ||| :

RESULT 13

S42881

platelet basic protein - pig

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Aug-1999

C:Accession: S43460; S42881

R: Power, C.A.; Proudfoot, A.E.I.; Magnenat, E.; Bacon, K.B.; Wells, T.N.C.

Eur. J. Biochem. 221, 713-719, 1994

A:Title: Molecular cloning and characterization of a neutrophil chemotactic protein f

A:Reference number: S43460; MUID:94229068

A:Accession: S43460

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-119 <POW>

A:Cross-references: EMBL:X77935; NID:g457753; PIDN:CAA54907.1; PID:g457754

C:Superfamily: beta-thromboglobulin

Query Match 55.4%; Score 210; DB 2; Length 119;

Best Local Similarity 56.7%; Pred. No. 1.4e-16;

Matches 38; Conservative 14; Mismatches 15; Indels 0; Gaps 0;

Qy 6 ELRCOCLOTLOGIHLKNIQSVKSPGPHCAQTEVIATLKNQKACLNPAASPMPVKKIIEX 65
: | |||||: | : ||||| | ||||| |||||: ||| : | : ||

Db 51 ELRCLCLNTVSGIHPSIOSLEVIKAGAHCAKVEVIATLKNKDKKICLDPEAPRIKKIVQK 110
: | |||||: | : ||||| | ||||| |||||: ||| : | : ||

Qy 66 MLKNGKS 72
: | : ||| :

Db 111 IMEDGGS 117
: | : ||| :

RESULT 14

TGHU

beta-thromboglobulin precursor [validated] - human

C:Species: Homo sapiens (man)

C:Date: 30-Apr-1979 #sequence_revision 31-Dec-1992 #text_change 08-Dec-2000

C:Accession: A39546; A37382; A24448; PLO222; A93982; A90411; A60709; A61240; B61240;

R: Majumdar, S.; Gonder, D.; Koutsis, B.; Poncz, M.

J. Biol. Chem. 266, 5785-5789, 1991

A:Title: Characterization of the human beta-thromboglobulin gene. Comparison with the

A:Reference number: A39546; MUID:91170256

A:Accession: A39546

A:Molecule type: DNA

A:Residues: 1-128 <MAJ>

A:Cross-references: GB:M54995; NID:g181175; PIDN:AAA62836.1; PID:g181176

A:Note: the authors translated the codon GAR for residue 109 as Pro

R: Wenger, R.H.; Wicki, A.N.; Walz, A.; Kieffer, N.; Clemetson, K.J.

Blood 73, 1498-1503, 1989

A:Title: Cloning of cDNA coding for connective tissue activating peptide III from a h

A:Reference number: A37382; MUID:89229374

A:Accession: A37382

A:Molecule type: mRNA

A:Residues: 1-128 <WEN>

A:Cross-references: GB:M54995; NID:g181175; PIDN:AAA62836.1; PID:g181176; GB:M38441

R: Holt, J.C.; Harris, M.E.; Holt, A.M.; Lange, E.; Henschen, A.; Niewiarowski, S.

Biochemistry 25, 1988-1996, 1986

A:Title: Characterization of human platelet basic protein, a precursor form of low-aff

A:Reference number: A24448; MUID:86216117

A:Accession: A24448

A:Molecule type: protein

A:Residues: 35-53 <HOL>

R: Walz, A.; Baggiolini, M.

J. Exp. Med. 171, 449-454, 1990

A:Title: Generation of the neutrophil-activating peptide NAP-2 from platelet basic pr

A:Reference number: PLO222; MUID:90155110

A:Accession: PLO222

A:Molecule type: protein

A:Residues: 54-67 <WAL>

A:Reference number: A60709; PMID:90237229
A:Accession: A60709
A:Molecule type: protein
A:Residues: 44-62,'X',64-79 <BAE>
A:Kaplan, A.P.; Baeza, M.; Reddigari, S.; Kuna, P.
J. Arch. Allergy Appl. Immunol. 94, 148-153, 1991
A:Title: Histamine-releasing factors.
A:Reference number: A61240; PMID:92040226
A:Accession: A61240
A:Molecule type: protein
A:Residues: 44-61,'XX',64 <KAP>
A:Accession: B61240
A:Molecule type: protein
A:Residues: 59-62,'X',64-79 <KA2>
R:Kungl, A.J.; Machius, M.; Huber, R.; Schwer, C.; Lam, C.; Aschauer, H.; Ehn, G.; Lindl
FEBS Lett. 347, 300-303, 1994
A:Title: Purification, crystallization and preliminary X-ray diffraction analysis of rec
A:Reference number: S46247; PMID:94307404
A:Contents: annotation
C:Comment: There appears to be a second beta-thromboglobulin-like human gene.
C:Comment: Connective-tissue activating peptides (CTAP) are a group of proteins capable
latelet, and polymorphonuclear leukocyte origin, respectively.
C:Comment: CTAP-III, a monomer isolated from platelets, stimulates DNA synthesis, mitosis
d sulfated glycosaminoglycan. It also stimulates the formation and secretion of plasmin
C:Comment: Proteolytic removal of the first four residues of CTAP-III produces the activ
ved growth factor.
C:Genetics:
A:Gene: GDB:PPBP; THBG1
A:Cross-references: GDB:127391; OMIM:121010
A:Map position: 4p12-q13
A:Introns: 50/1; 95/2
C:Superfamily: beta-thromboglobulin
Keywords: growth factor; homotetramer; platelet
34/Domain: signal sequence #status predicted <SIG>
35-43/Domain: propeptide #status predicted <PRO>
F:44-128/Product: connective-tissue activating peptide III #status experimental <CTAP>
F:48-128/Product: beta-thromboglobulin #status experimental <BTG>
F:59-128/Product: neutrophil-activating peptide 2 #status experimental <NAP2>
F:63-89,65-105/Disulfide bonds: #status experimental

Query Match	54.98;	Score 208;	DB 2;	Length 75;
Best Local Similarity	50.0%;	Pred. No. 1.4e-16;		
Matches	36;	Conservative 18;	Mismatches 18;	Indels 0; Gaps 0;
Qy	1	APLATELRCCQLQFLQGIHLKNIQSVKSPGPHCAQTEVIATILKNGOKACLNPAASPMVK	60	
		: : : : : : : : :		
Db	4	AAVRELRCVGLTTTPGTHPTVSDLVQIAGPQCSKVEVIATILKNGREVCLDPEAPLIK	63	
Qy	61	KIIEKMLKNGKS	72	
		: : : : :		
Db	64	KIVOKILDSGN	75	

Search completed: May 4, 2001, 07:36:24
Job time: 56 sec

RESULT 15
B54188

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 4, 2001, 07:35:28 ; Search time 9.61 Seconds
(without alignments)
260.213 Million cell updates/sec

Title: US-09-467-160-3

Perfect score: 379

Sequence: 1 AFLATLRCQLTQLOGIHL.....PASPMVKIIEKMLKNGKSN 73

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	379	100.0	107	1	M12A_HUMAN
2	331	87.3	107	1	GRO_HUMAN
3	325	85.8	107	1	M12B_HUMAN
4	304	80.2	101	1	GRO_CRIGR
5	304	80.2	103	1	GRO_SHEEP
6	300	79.2	98	1	GRO_BOVIN
7	299	78.9	104	1	GROA_BOVIN
8	299	78.9	104	1	GROB_BOVIN
9	296	78.1	71	1	GRO1_RABIT
10	295	77.8	104	1	GRO2_RABIT
11	284	74.9	96	1	GRO_MOUSE
12	278	73.4	96	1	GRO_MOUSE
13	261	68.9	100	1	MIP2_MOUSE
14	257	67.8	104	1	GRO_CAVPO
15	249	65.7	100	1	MIP2_RAT
16	237	62.5	68	1	M12A_RAT
17	233	61.5	100	1	M12B_RAT
18	210	55.4	117	1	AMC2_PIG
19	210	55.4	119	1	PF4L_PIG
20	209	55.1	128	1	PF4L_HUMAN
21	208	54.9	75	1	SZ06_BOVIN
22	199.5	52.6	114	1	SZ05_HUMAN
23	176.5	46.6	103	1	EMF1_CHICK
24	174	45.9	114	1	SZ06_HUMAN
25	173	45.6	85	1	PLF4_SHEEP
26	173	45.6	90	1	PLF4_PIG
27	168	44.3	125	1	SZ09_HUMAN
28	166.5	43.9	101	1	IL8_MACMU
29	166.5	43.9	101	1	PLF4_RAT
30	164.5	43.4	99	1	IL8_HUMAN
31	164.5	43.4	101	1	IL8_CERTO
32	163	43.0	132	1	SZ05_MOUSE
33	162.5	42.9	130	1	SZ05_RAT

34	160	42.2	101	1	PLF4_HUMAN	P02776	homo sapien
35	160	42.2	126	1	SZ09_MOUSE	P18340	mus musculus
36	155.5	41.0	101	1	IL8_BOVIN	P79255	bos taurus
37	155.5	41.0	101	1	IL8_SHEEP	P36925	ovis aries
38	151	39.8	88	1	PLF4_BOVIN	P02777	bos taurus
39	150.5	39.7	101	1	IL8_RABIT	P19874	oryctolagus
40	146.5	38.7	101	1	IL8_CANFA	P41324	canis famill
41	146.5	38.7	103	1	IL8_PIG	P26894	sus scrofa
42	142	37.5	104	1	PLFV_HUMAN	O62812	homo sapien
43	138.5	36.5	97	1	IL8_HORSE	P02778	equus caball
44	130.5	34.4	101	1	IL8_CAVPO	P49113	cavia porce
45	113	29.8	98	1	SZ10_HUMAN		homo sapien

ALIGNMENTS

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RESULT 1
M12A_HUMAN
ID M12A_HUMAN STANDARD; PRT; 107 AA.
AC P19875: O9UPB8;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DE MACROPHAGE INFLAMMATORY PROTEIN-2-ALPHA PRECURSOR (MIP2-ALPHA) (GROWTH
DE REGULATED PROTEIN BETA) (GRO-BETA).
GN GRO2 OR GROB OR MIP2A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Histocytic lymphoma;
RX MEDLINE=90354792; PubMed=2201751;
RA Tekamp-Olson P., Gallegos C., Bauer D., McClain J., Sherry B.,
RA Fabre M., van Deventer S., Cerami A.;
RT "Cloning and characterization of cDNAs for murine macrophage
RT inflammatory protein 2 and its human homologues.";
RL J. Exp. Med. 172:911-919(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90377259; PubMed=2078213;
RA Iida N., Grotendorst G.R.;
RT "Cloning and sequencing of a new gro transcript from activated human
RT monocytes: expression in leukocytes and wound tissue.";
RL Mol. Cell. Biol. 10:5596-5599(1990).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=91017578; PubMed=2217207;
RA Haskill S., Peace A., Morris J., Sporn S.A., Anisowicz A., Lee S.W.,
RA Smith T., Martin G., Ralph P., Sager R.;
RT "Identification of three related human GRO genes encoding cytokine
RT functions";
RL Proc. Natl. Acad. Sci. U.S.A. 87:7732-7736(1990).
RN [4]
RP SEQUENCE OF 35-107 FROM N.A.
RA Jang J.S., Kim B.E.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [5]
RP STRUCTURE BY NMR OF 39-107.
RX MEDLINE=20069929; PubMed=10600366;
RA Qian Y.Q., Johanson K.O., McDewitt P.;
RT "Nuclear magnetic resonance solution structure of truncated human
RT GRObeta [5-73] and its structural comparison with CXK chemokine
RT family members GROalpha and IL-8.";
RL J. Mol. Biol. 294:1085-1072(1999).
CC -!- FUNCTION: PRODUCED BY ACTIVATED
CC EXPRESSED AT SITES OF INFLAMMATION.
CC -!- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
CC C-X-C) (CHEMOKINE CXK).
-----
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DR EMBL; X53799; CAA37808.1; -;
 DR EMBL; M36820; AAG3183.1; -;
 DR EMBL; M57731; AAG3182.1; -;
 DR EMBL; AF043340; AAC03540.1; -;
 DR PIR; JH0281; JH0281;
 DR PDB; 1QNK; 04-FEB-00.
 DR MIM; 139110; -;
 DR InterPro; IPR001089; -;
 DR InterPro; IPR001811; -;
 DR InterPro; IPR002473; -;
 DR Pfam; PF00048; IL8; 1;
 DR PRINTS; PR00436; INTERLEUKIN8;
 DR PRINTS; PR00437; SMALLCYTOKINE;
 DR PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1;
 DR Cytokine; Chemotaxis; Inflammatory response; Signal; 3D-structure.
 DR SIGNAL 1 34
 DR CHAIN 35 107 MACROPHAGE INFLAMMATORY PROTEIN-
 DR 2-ALPHA.

FT DISULFID 43 69
 FT DISULFID 45 85
 SQ SEQUENCE 107 AA; 11389 MW; 740F277E928571BA CRC64;

Query Match 100.0%; Score 379; DB 1; Length 107;
 Best Local Similarity 100.0%; Pred. No. 2.4e-36;
 Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 APLATELCOCLOTLOGIHLKNIQSVKSPGPHCAQTEVIATLKNGOKACLNAPSPMKV 60
 DB 35 APLATELCOCLOTLOGIHLKNIQSVKSPGPHCAQTEVIATLKNGOKACLNAPSPMKV 94
 OY 61 KIIEKMLKNGKSN 73
 DB 95 KIIEKMLKNGKSN 107

RESULT 2
 GRO_HUMAN STANDARD; PRT; 107 AA.
 ID GRO_HUMAN
 AC P09341;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DT GROWTH REGULATED PROTEIN PRECURSOR (MELANOMA GROWTH STIMULATORY
 ACTIVITY) (MGSA) (NEUTROPHIL-ACTIVATING PROTEIN 3) (NAP-3).
 GN SCYB1 OR GRO1 OR GROA OR GRO OR MGSA.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88041072; PubMed=2890161;
 RA Anisowicz A., Bardwell L., Sager R.;
 RT "Constitutive overexpression of a growth-regulated gene in
 RT transformed Chinese hamster and human cells";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:7188-7192(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88328991; PubMed=2970963;
 RA Richmond A., Balentien E., Thomas H.G., Flagg G., Barton D.E.,
 RA Spiess J., Bordon R., Francke U., Derynck R.;
 RT "Molecular characterization and chromosomal mapping of melanoma
 RT growth stimulatory activity, a growth factor structurally related to
 RT beta-thromboglobulin";
 RL EMBO J. 7:2025-2033(1988).
 DR

RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RX MEDLINE=91057157; PubMed=2129556;
 RA Baker N.E., Kucera G., Richmond A.;
 RT "Nucleotide sequence of the human melanoma growth stimulatory
 RT activity (MGSA) gene";
 RL Nucleic Acids Res. 18:6453-6453(1990).
 RN [4]
 RP SEQUENCE OF 35-65.
 RX MEDLINE=90217938; PubMed=2182761;
 RA Schroeder J.-M., Persoon N.L.M., Christophers E.;
 RT "Lipopolysaccharide-stimulated human monocytes secrete, apart from
 RT neutrophil-activating peptide 1/interleukin 8, a second neutrophil-
 RT activating protein. NH2-terminal amino acid sequence identity with
 RT melanoma growth stimulatory activity";
 RL J. Exp. Med. 171:1091-1100(1990).
 RN [5]
 RP SEQUENCE OF 35-57.
 RX MEDLINE=89246368; PubMed=2655583;
 RA Golds E.E., Mason P., Nyirkos P.;
 RT "Inflammatory cytokines induce synthesis and secretion of gro protein
 RT and a neutrophil chemotactic factor but not beta 2-microglobulin in
 RT human synovial cells and fibroblasts";
 RL Biochem. J. 259:585-588(1989).
 RN [6]
 RP POSSIBLE FUNCTION.
 RX MEDLINE=89356650; PubMed=2670560;
 RA Wen D., Rowland A., Derynck R.;
 RT "Expression and secretion of gro/MGSA by stimulated human endothelial
 RT cells";
 RL EMBO J. 8:1761-1766(1989).
 RN [7]
 RP STRUCTURE BY NMR.
 RX MEDLINE=93387459; PubMed=83971104;
 RA Fairbrother W.J., Reilly D., Colby T., Horuk R.;
 RT "1H assignment and secondary structure determination of human
 RT melanoma growth stimulating activity (MGSA) by NMR spectroscopy";
 RL FEBS Lett. 330:302-306(1993).
 RN [8]
 RP STRUCTURE BY NMR.
 RX MEDLINE=94376296; PubMed=8089846;
 RA Fairbrother W.J., Reilly D., Colby T., Hesselgesser J., Horuk R.;
 RT "The solution structure of melanoma growth stimulating activity";
 RL J. Mol. Biol. 242:252-270(1994).
 RN [9]
 RP STRUCTURE BY NMR.
 RX MEDLINE=95105175; PubMed=7806518;
 RA Kim K.S., Clark-Lewis I., Sykes B.D.;
 RT "Solution structure of GRO/melanoma growth stimulatory activity
 RT determined by 1H NMR spectroscopy";
 RL J. Biol. Chem. 269:32909-32915(1994).
 CC -1- FUNCTION: HAS CHEMOTACTIC ACTIVITY FOR NEUTROPHILS. MAY PLAY A
 CC ROLE IN INFLAMMATION AND EXERTS ITS EFFECTS ON ENDOTHELIAL CELLS
 CC IN AN AUTOCRINE FASHION.
 CC -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
 CC C-X-C) (CHEMOKINE CXC).
 CC -----
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 CC -----
 DR EMBL; J03561; AAA35933.1; -;
 DR EMBL; X12510; CAA31027.1; -;
 DR EMBL; X54489; CAA38361.1; -;
 DR PIR; A28414; A28414.
 DR PIR; S00983; S00983.
 DR PIR; S03976; S03976.
 DR PIR; S13669; S13669.
 DR

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DR PDB; 1MGS; 30-SEP-94.
DR PDB; 1MSG; 31-MAR-95.
DR PDB; 1MSH; 31-MAR-95.
DR MIM; 155730; -.
DR InterPro; IPR001089; -.
DR InterPro; IPR001811; -.
DR InterPro; IPR002473; -.
DR Pfam; PF00048; IL8; 1.
DR PRINTS; PR00436; INTERLEUKIN8.
DR PROSITE; PS00471; SMALL_CYTOKINES_CXC.
KW Cytokine; Growth factor; Inflammatory response; Signal; 3D-structure.
FT CHAIN 35 107 GROWTH REGULATED PROTEIN.
FT DISULFID 43 69
FT DISULFID 45 85
SQ SEQUENCE 107 AA; 11301 MW; 17048A6B4D765CA2 CRC64;

Query Match 87.3%; Score 331; DB 1; Length 107;
Best Local Similarity 87.7%; Pred. No. 6,8e-31;
Matches 64; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 APLATELRQCQCLQTLOGIHLKNIQSVKSPGPHCAQTEVIATLKNQKACLNPA5PMVK 60
| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 35 ASVATELRQCQCLQTLOGIHLKNIQSVKSPGPHCAQTEVIATLKNQKACLNPA5PIVK 94

QY 61 KIIEKMLNKGKSN 73
| ||||| : |||
DB 95 KIIEKMLNKGKSN 107

RESULT 3
MI2B_HUMAN
ID MI2B_HUMAN STANDARD; PRT; 107 AA.
AC P19876;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE MACROPHAGE INFLAMMATORY PROTEIN-2-BETA PRECURSOR (MIP2-BETA) (GROWTH
DE REGULATED PROTEIN GAMMA) (GRO-GAMMA).
GN GRO3 OR GROG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
PY [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Histiocytic lymphoma;
RX MEDLINE=90354792; PubMed=2201751;
RA Tekamp-Olson P., Gallegos C., Bauer D., McClain J., Sherry B.,
RA Fabre M., van Deventer S., Cerami A.;
RT "Cloning and characterization of cDNAs for murine macrophage
RT inflammatory protein 2 and its human homologues.";
RL J. Exp. Med. 172:911-919(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91017578; PubMed=2217207;
RA Haskill S., Pearce A., Morris J., Sporn S.A., Anisowicz A., Lee S.W.,
RA Smith T., Martin G., Ralph P., Sager R.;
RT "Identification of three related human GRO genes encoding cytokine
RT functions.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:7732-7736(1990).
CC -!- FUNCTION: MAY PLAY A ROLE IN INFLAMMATION AND EXERT ITS EFFECTS
CC ON ENDOTHELIAL CELLS IN AN AUTOCRINE FASHION.
CC -!- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
CC C-X-C) (CHEMOKINE CXC).
CC
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CC
CC EMBL; X53800; CAA37809.1; -.
CC EMBL; M36821; AAA63184.1; -.
DR PIR; B38290; B38290.
DR PIR; JH0282; JH0282.
DR HSSP; P09341; 1MGS.
DR MIM; 139111; -.
DR InterPro; IPR001089; -.
DR InterPro; IPR001811; -.
DR InterPro; IPR002473; -.
DR Pfam; PF00048; IL8; 1.
DR PRINTS; PR00436; INTERLEUKIN8.
DR PROSITE; PS00437; SMALLCYTKCXC.
KW Cytokine; Chemotaxis; Inflammatory response; Signal.
FT SIGNAL 1 34
FT CHAIN 35 107 MACROPHAGE INFLAMMATORY PROTEIN-
FT 2-BETA.
FT DISULFID 43 69 BY SIMILARITY.
FT DISULFID 45 85 BY SIMILARITY.
FT CONFLICT 27 28 AA -> G (IN REF. 2).
SQ SEQUENCE 107 AA; 11342 MW; 97A69946B7F1F070 CRC64;

Query Match 85.8%; Score 325; DB 1; Length 107;
Best Local Similarity 83.6%; Pred. No. 3.2e-30;
Matches 61; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 APLATELRQCQCLQTLOGIHLKNIQSVKSPGPHCAQTEVIATLKNQKACLNPA5PMVK 60
| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 35 ASVATELRQCQCLQTLOGIHLKNIQSVKSPGPHCAQTEVIATLKNQKACLNPA5PMVQ 94

QY 61 KIIEKMLNKGKSN 73
| ||||| : |||
DB 95 KIIEKMLNKGKSN 107

RESULT 4
GRO_CRIGR STANDARD; PRT; 101 AA.
AC P09340;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE GROWTH REGULATED PROTEIN PRECURSOR.
GN SCYB1 OR GRO.
OS Cricetus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetulus.
OX NCBI_TaxID=10029;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88041072; PubMed=2890161;
RA Anisowicz A., Bardwell L., Sager R.;
RT "Constitutive overexpression of a growth-regulated gene in
RT transformed Chinese hamster and human cells.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:7188-7192(1987).
CC -!- FUNCTION: HAS CHEMOTACTIC ACTIVITY FOR NEUTROPHILS.
CC -!- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
CC C-X-C) (CHEMOKINE CXC).
CC
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CC
CC EMBL; J03560; AAA36985.1; -.

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FT	CHAIN	31	103	GROWTH REGULATED PROTEIN.	
FT	DISULFID	39	65	BY SIMILARITY.	
FT	DISULFID	41	81	BY SIMILARITY.	
SQ	SEQUENCE	103 AA;	10820 MW;	C59857F346716695	CRC64;
Query Match 80.2%; Score 304; DB 1; Length 103;					
Best Local Similarity 76.7%; Pred. No. 7.5e-28;					
Matches 56; Conservative 6; Mismatches 11; Indels 0; Gaps 0;					
Qy	1 APLATELRCCQLQTLOGIHLNKIQSVKSPGPHCAQTEVIATLKGOKACLNPAAPMKV 60				
Db	31 APVYNELRCQCLQTQVGIHLNKMQSVKTPPGPHCGQTEVIATLKTGQVCLNPAAPMKV 90				
Qy	61 KIIKMLKNGKSN 73				
Db	91 KIIKMLNQAASN 103				
RESULT 6					
ID	GROG_BOVIN	STANDARD;	PRT;	98 AA.	
AC	O46675;				
DT	15-DEC-1998 (Rel. 37, Created)				
DT	15-DEC-1998 (Rel. 37, Last sequence update)				
DT	15-DEC-1998 (Rel. 37, Last annotation update)				
DE	GROWTH REGULATED PROTEIN HOMOLOG GAMMA PRECURSOR (GRO-GAMMA).				
OS	Bos taurus (Bovine).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;				
OC	Bovidae; Bovinae; Bos.				
OX	NCBI_Taxid-9913;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RL	Yoshimura T., Modi W.S.;				
RL	Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.				
CC	-!- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE				
CC	C-X-C) (CHEMOKINE CXCL).				
CC	-----				
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CC	or send an email to license@isb-sib.ch).				
CC	-----				
DR	EMBL; U95811; AAB93927.1; ..				
DR	InterPro; IPR001089; ..				
DR	InterPro; IPR001811; ..				
DR	Pfam; PF00048; IL8; 1.				
DR	PRINTS; PR00437; SMALLCYTRXCX.				
DR	PROSITE; PS00471; SMALLCYTRKNCX; 1.				
KW	Cytokine; Growth factor; Inflammatory response; Signal.				
FT	SIGNAL	1	29	POTENTIAL.	
FT	CHAIN	30	98	GROWTH REGULATED PROTEIN HOMOLOG GAMMA.	
FT	DISULFID	39	65	BY SIMILARITY.	
FT	DISULFID	41	81	BY SIMILARITY.	
SQ	SEQUENCE	98 AA;	10393 MW;	942CD6897C21EDE9	CRC64;
Query Match 79.2%; Score 300; DB 1; Length 98;					
Best Local Similarity 83.6%; Pred. No. 2e-27;					
Matches 56; Conservative 5; Mismatches 6; Indels 0; Gaps 0;					
Qy	1 APLATELRCCQLQTLOGIHLNKIQSVKSPGPHCAQTEVIATLKGOKACLNPAAPMKV 60				
Db	31 APVYNELRCQCLQTLOGIHLNKMQSVKTPPGPHCDQTEVIATLKTGQVCLNPAAPMKV 90				
Qy	61 KIIKML 67				
Db	91 KIIKML 97				

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RESULT 7
GROB_BOVIN
ID GROB_BOVIN STANDARD; PRT; 104 AA.
AC O46676;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE GROWTH REGULATED PROTEIN HOMOLOG ALPHA PRECURSOR (GRO-ALPHA).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovoidea; Bovinae; Bos.
OC NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
Yoshimura T., Modi W.S.;
Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
-!- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
C-X-C) (CHEMOKINE CXCL)
-----
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-----
DR EMBL; U95812; AAB93928.1; -
DR InterPro; IPR001089; -
DR InterPro; IPR001811; -
DR InterPro; IPR002473; -
DR Pfam; PF00048; IL8; 1.
DR PRINTS; PR00436; INTERLEUKIN8.
DR PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
DR CYTOKINE; Growth factor; Inflammatory response; Signal.
FT SIGNAL 1 30 POTENTIAL.
FT CHAIN 31 104 GROWTH REGULATED PROTEIN HOMOLOG ALPHA.
FT DISULFID 40 66 BY SIMILARITY.
FT DISULFID 42 82 BY SIMILARITY.
SQ SEQUENCE 104 AA; 10984 MW; 1002CAC064DB1F76 CRC64;
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Query Match 78.9%; Score 299; DB 1; Length 104;
Best Local Similarity 75.3%; Pred. No. 2.8e-27;
Matches 55; Conservative 7; Mismatches 11; Indels 0; Gaps 0;
QY 1 APLATELRCCQCLTQLOGIHLKNIQSVKSPGPHCAQTEVIATLKNQKACLNAPSPMWK 60
DB 32 APVNELRCCQCLTQLOGIHLKNIQSVKVTTPGPHCDQTEVIASLTQGEVCLNPTAPMWK 91
QY 61 KIIEKMLKNGKSN 73
DB 92 KIIDKMLNKASAN 104
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RESULT 8
GROB_BOVIN
ID GROB_BOVIN STANDARD; PRT; 104 AA.
AC O46677;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE GROWTH REGULATED PROTEIN HOMOLOG BETA PRECURSOR (GRO-BETA).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovoidea; Bovinae; Bos.
OC NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
Yoshimura T., Modi W.S.;
Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
-!- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
C-X-C) (CHEMOKINE CXCL)
-----
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-----
DR EMBL; U95812; AAB93928.1; -
DR InterPro; IPR001089; -
DR InterPro; IPR001811; -
DR InterPro; IPR002473; -
DR Pfam; PF00048; IL8; 1.
DR PRINTS; PR00436; INTERLEUKIN8.
DR PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
DR CYTOKINE; Growth factor; Inflammatory response; Signal.
FT SIGNAL 1 30 POTENTIAL.
FT CHAIN 31 104 GROWTH REGULATED PROTEIN HOMOLOG ALPHA.
FT DISULFID 40 66 BY SIMILARITY.
FT DISULFID 42 82 BY SIMILARITY.
SQ SEQUENCE 104 AA; 10984 MW; 1002CAC064DB1F76 CRC64;
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Query Match 78.9%; Score 299; DB 1; Length 104;
Best Local Similarity 75.3%; Pred. No. 2.8e-27;
Matches 55; Conservative 7; Mismatches 11; Indels 0; Gaps 0;
QY 1 APLATELRCCQCLTQLOGIHLKNIQSVKSPGPHCAQTEVIATLKNQKACLNAPSPMWK 60
DB 32 APVNELRCCQCLTQLOGIHLKNIQSVKVTTPGPHCDQTEVIASLTQGEVCLNPTAPMWK 91
QY 61 KIIEKMLKNGKSN 73
DB 92 KIIDKMLNKASAN 104
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RESULT 9
GROB_BOVIN
ID GROB_BOVIN STANDARD; PRT; 71 AA.
AC P30782;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE PERMEABILITY FACTOR 2 (RPF2) (FRAGMENT).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OC NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-NEW ZEALAND WHITE; TISSUE=Alveolar macrophage;
RX MEDLINE=95129889; PubMed=7828903;
RA Johnson M.C., Goodman R.B. II, Kajikawa O., Wong V.A., Mongovin S.M.,
RA Martin T.R.;
RT "Cloning of two rabbit GRO homologues and their expression in
RT alveolar macrophages.";
RL Gene 151:337-338(1994).
RN [2]
RP SEQUENCE OF 1-36.
RC STRAIN-NEW ZEALAND WHITE; TISSUE=Peritoneal cavity;
RX MEDLINE=91378900; PubMed=1898341;
RA Jose P.J., Collins P.D., Perkins J.A., Beaubien B.C., Totty N.F.,
RA Waterfield M.D., Hsuan J., Williams T.J.;
RT "Identification of a second neutrophil-chemoattractant cytokine
RT generated during an inflammatory reaction in the rabbit peritoneal
RT cavity in vivo. Purification, partial amino acid sequence and
RT structural relationship to melanoma-growth-stimulatory activity.";
```

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RA Yoshimura T., Modi W.S.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
-!- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
C-X-C) (CHEMOKINE CXCL)
-----
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-----
DR EMBL; U95813; AAB93929.1; -
DR InterPro; IPR001089; -
DR InterPro; IPR001811; -
DR InterPro; IPR002473; -
DR Pfam; PF00048; IL8; 1.
DR PRINTS; PR00436; INTERLEUKIN8.
DR PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
DR CYTOKINE; Growth factor; Inflammatory response; Signal.
FT SIGNAL 1 30 POTENTIAL.
FT CHAIN 31 104 GROWTH REGULATED PROTEIN HOMOLOG BETA.
FT DISULFID 40 66 BY SIMILARITY.
FT DISULFID 42 82 BY SIMILARITY.
SQ SEQUENCE 104 AA; 10950 MW; 40A8C06A64D67F7B CRC64;
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Query Match 78.9%; Score 299; DB 1; Length 104;
Best Local Similarity 75.3%; Pred. No. 2.8e-27;
Matches 55; Conservative 7; Mismatches 11; Indels 0; Gaps 0;
QY 1 APLATELRCCQCLTQLOGIHLKNIQSVKSPGPHCAQTEVIATLKNQKACLNAPSPMWK 60
DB 32 APVNELRCCQCLTQLOGIHLKNIQSVKVTTPGPHCDQTEVIASLTQGEVCLNPTAPMWK 91
QY 61 KIIEKMLKNGKSN 73
DB 92 KIIDKMLNKASAN 104
-----
RESULT 9
GROB_BOVIN
ID GROB_BOVIN STANDARD; PRT; 71 AA.
AC P30782;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE PERMEABILITY FACTOR 2 (RPF2) (FRAGMENT).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OC NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-NEW ZEALAND WHITE; TISSUE=Alveolar macrophage;
RX MEDLINE=95129889; PubMed=7828903;
RA Johnson M.C., Goodman R.B. II, Kajikawa O., Wong V.A., Mongovin S.M.,
RA Martin T.R.;
RT "Cloning of two rabbit GRO homologues and their expression in
RT alveolar macrophages.";
RL Gene 151:337-338(1994).
RN [2]
RP SEQUENCE OF 1-36.
RC STRAIN-NEW ZEALAND WHITE; TISSUE=Peritoneal cavity;
RX MEDLINE=91378900; PubMed=1898341;
RA Jose P.J., Collins P.D., Perkins J.A., Beaubien B.C., Totty N.F.,
RA Waterfield M.D., Hsuan J., Williams T.J.;
RT "Identification of a second neutrophil-chemoattractant cytokine
RT generated during an inflammatory reaction in the rabbit peritoneal
RT cavity in vivo. Purification, partial amino acid sequence and
RT structural relationship to melanoma-growth-stimulatory activity.";
```

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CC      -----
EMBL; UI2310; AAA20487.1; -.
HSP; P09341; LMGS.
InterPro: IPR001089; -.
InterPro: IPR001811; -.
InterPro: IPR002473; -.
Pfam; PF00048; IL8; 1.
PRINTS; PR00436; INTERLEUKIN8.
PRINTS; PR00437; SMALLCYTOKINE.
PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
KW      Cytokine; Growth factor; Inflammatory response; Signal.
FT      SIGNAL 1 31 PROBABLE.
FT      CHAIN 32 104 GROWTH REGULATED PROTEIN HOMOLOG.
FT      DISULFID 40 66 BY SIMILARITY.
FT      DISULFID 42 82 BY SIMILARITY.
FT      SEQUENCE 104 AA; 10900 MW; 10B9D07B65C77F67 CRC64;
SQ
Query Match 77.8%; Score 295; DB 1; Length 104;
Best Local Similarity 74.0%; Pred. No. 7.9e-27;
Matches 54; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 1 APLATELRCCQLQTLQGIHLKNIQSVKSGPGHCAOTEVIATLKNGKACLNPA5PWVK 60
Db 32 APVYNELRCCLQTLQGIHLKNIQSVKVTTPGPHCDQTEVIASLKTGOEVLNPTAPVK 91
QY 61 KIIEKMLKNGKSN 73
Db 92 KIIDKMLNKASAN 104

RESULT 11
GRO_RAT
ID GRO_RAT STANDARD; PRT; 96 AA.
AC P14095;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE GROWTH REGULATED PROTEIN PRECURSOR (CYTOKINE-INDUCED NEUTROPHIL
DE CHEMOATTRACTANT) (CINC-1) (PLATELET-DERIVED GROWTH FACTOR-INDUCIBLE
DE PROTEIN KC).
DE SCYB1 OR GRO.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RN MEDLINE=93246259; PubMed=8482545;
RA Konishi K., Tanaka Y., Yamamoto M., Yomogida K., Watanabe K.,
RA Tsurufuji S., Fujioaka M.;
RA "Structure of the gene encoding rat neutrophil chemo-attractant Gro.";
RL Gene 126:285-286(1993).
RN [2]
RN SEQUENCE FROM N.A.
RN MEDLINE=92246987; PubMed=1374243;
RX Huang S., Paulauskis J., Kobzik L.;
RA "Rat KC cDNA cloning and mRNA expression in lung macrophages and
RA fibroblasts.";
RL Biochem. Biophys. Res. Commun. 184:922-929(1992).
RN [3]
RN SEQUENCE OF 25-96.
RX MEDLINE=90062049; PubMed=2684956;
RA Watanabe K., Konishi K., Fujioaka M., Kinoshita S., Nakagawa H.;
RA "The neutrophil chemoattractant produced by the rat kidney
RA epithelioid cell line NRK-52E is a protein related to the KC/gro
RA protein.";
RL J. Biol. Chem. 264:19559-19563(1989).
RN [4]
RN SEQUENCE OF 36-88 FROM N.A.
RX TISSUE=Lung;
RX MEDLINE=93035653; PubMed=1415488;

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RA Huang S., Paulauskis J.D., Godleski J.J., Kobzik L.;
 RT "Expression of macrophage inflammatory protein-2 and KC mRNA in
 RT pulmonary inflammation.";
 RL Am. J. Pathol. 141:981-988(1992).
 RN [5]
 RP SEQUENCE OF 25-56.
 RC STRAIN=WISTAR;
 RX MEDLINE=96183056; PubMed=8607872;
 RA Nakagawa H., Shiota S., Takano K., Shibata F., Kato H.;
 RT "Cytokine-induced neutrophil chemoattractant (CINC)-2 alpha, a novel
 RT member of rat GRO/CINCs, is a predominant chemokine produced by
 RT lipopolysaccharide-stimulated rat macrophages in culture.";
 RL Biochem. Biophys. Res. Commun. 220:945-948(1996).
 RN [6]
 RP STRUCTURE BY NMR.
 RX MEDLINE=95046335; PubMed=7957925;
 RA Hanzawa H., Hanyama H., Watanabe K., Tsurufuji S.;
 RT "The three dimensional structure of rat cytokine CINC/gro in solution
 RT by homonuclear 3D NMR.";
 RL FEBS Lett. 354:207-212(1994).
 RN [7]
 RP STRUCTURE BY NMR.
 RX MEDLINE=97335927; PubMed=9192722;
 RA Hanzawa H., Hanyama H., Konishi K., Watanabe K., Tsurufuji S.;
 RT "Subunit association and monomer structure of CINC/Gro revealed by
 RT 1H-NMR.";
 RL J. Biochem. 121:835-841(1997).
 RN [8]
 RP STRUCTURE BY NMR.
 RX MEDLINE=98162936; PubMed=9504410;
 RA Hanzawa H., Hanyama H., Konishi K., Watanabe K., Tsurufuji S.;
 RT "Solution structure of CINC/Gro investigated by heteronuclear NMR.";
 RL J. Biochem. 123:62-70(1998).
 CC -!- FUNCTION: HAS CHEMOTACTIC ACTIVITY FOR NEUTROPHILS. CONTRIBUTES TO
 CC NEUTROPHIL ACTIVATION DURING INFLAMMATION.
 CC -!- SUBUNIT: MONOMER AND HOMODIMER.
 CC -!- TISSUE SPECIFICITY: AT LEAST EXPRESSED IN THE LUNG AND TRACHEA.
 CC -!- INDUCTION: IN LUNG, BY LIPOPOLYSACCHARIDE OR INFLAMMATION.
 CC -!- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
 CC C-X-C) (CHEMOKINE CX-C).
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 CC -----
 CC EMBL; D11445; BAA02009.1; -;
 CC EMBL; D11444; BAA02008.1; -;
 CC EMBL; M86536; AAA42053.1; -;
 CC EMBL; S45856; -; NOT_ANNOTATED_CDS.
 CC PIR; A34481; A34481.
 CC HSP; P09341; IWSH.
 CC InterPro; IPR001089; -;
 CC InterPro; IPR001811; -;
 CC InterPro; IPR002473; -;
 CC Pfam; PF00048; IL8; 1.
 CC PRINTS; PR00436; INTERLEUKIN8.
 CC PRINTS; PR00437; SMALLCYTOKINE.
 CC PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
 CC Cytokine; Growth factor; Inflammatory response; Signal.
 CC SIGNAL 1 24
 CC CHAIN 25 96 GROWTH REGULATED PROTEIN.
 CC DISULFID 33 59 BY SIMILARITY.
 CC DISULFID 35 75 BY SIMILARITY.
 CC SEQUENCE 96 AA; 10249 MW; 6046C9E2C2582652 CRC64;
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 CC -----
 CC EMBL; J04596; AAA40131.1; -;
 CC EMBL; U20634; AAB03376.1; -;
 CC EMBL; U20527; AAB03376.1; JOINED.
 CC EMBL; S79767; -; NOT_ANNOTATED_CDS.
 CC PIR; A32954; A32954.
 CC PIR; JH0081; JH0081.

Query Match 74.98; Score 284; DB 1; Length 96;
 Best Local Similarity 75.08; Pred. No. 1.3e-25;
 Matches 51; Conservative 10; Mismatches 7; Indels 0; Gaps 0;

QY 1 APLATELRCCQLTQLOGLHKLNTQSVKVGSPGPHCAQTEVIATLKNQKACLNPASPMVK 60
 DB 25 APVANELRCQLQTVAGIHFKNIQSLKVMPPGPHCTQTEVIATLKNQKREACLDPEADPMVQ 84
 QY 61 KIIEKMLK 68
 DB 85 KIVQKMLK 92
 RESULT 12
 GRO_MOUSE STANDARD; PRT; 96 AA.
 AC P12850;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DE 01-OCT-2000 (Rel. 40, Last annotation update)
 DE GROWTH REGULATED PROTEIN PRECURSOR (PLATELET-DERIVED GROWTH FACTOR-
 DE INDUCIBLE PROTEIN KC) (SECRETORY PROTEIN N51).
 GN SCYB1 OR GRO1 OR GRO OR MGSA.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89139485; PubMed=2917992;
 RA Quendo P., Alberta J., Wen D., Graycar J.L., Derynck R., Stiles C.D.;
 RT "The platelet-derived growth factor-inducible KC gene encodes a
 RT secretory protein related to platelet alpha-granule proteins.";
 RL J. Biol. Chem. 264:4133-4137(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89078502; PubMed=2909392;
 RA Ryseck R.P., Macdonald-Bravo H., Mattei M.-G., Bravo R.;
 RT "Cloning and sequence of a secretory protein induced by growth
 RT factors in mouse fibroblasts.";
 RL Exp. Cell Res. 180:266-275(1989).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96016008; PubMed=7561058;
 RA Ohmori Y., Fukumoto S., Hamilton T.A.;
 RT "Two structurally distinct kappa B sequence motifs cooperatively
 RT control LPS-induced KC gene transcription in mouse macrophages.";
 RL J. Immunol. 155:3593-3600(1995).
 CC -!- FUNCTION: HAS CHEMOTACTIC ACTIVITY FOR NEUTROPHILS. CONTRIBUTES TO
 CC NEUTROPHIL ACTIVATION DURING INFLAMMATION (BY SIMILARITY).
 CC -!- INDUCTION: BY PLATELET-DERIVED GROWTH FACTOR. IN LUNG, BY
 CC LIPOPOLYSACCHARIDE OR INFLAMMATION (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
 CC C-X-C) (CHEMOKINE CX-C).
 CC -----
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 CC -----
 CC EMBL; J04596; AAA40131.1; -;
 CC EMBL; U20634; AAB03376.1; -;
 CC EMBL; U20527; AAB03376.1; JOINED.
 CC EMBL; S79767; -; NOT_ANNOTATED_CDS.
 CC PIR; A32954; A32954.
 CC PIR; JH0081; JH0081.

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CC EMBL; X53798; CAA37807.1; -.  
DR DR PIR; JH0200; JH0200.  
DR PDB; 1M12; 29-APR-98.  
DR MGD; MGI:1340094; Scyb2.  
DR InterPro; IPR001089; -.  
DR InterPro; IPR001811; -.  
DR InterPro; IPR002473; -.  
DR Pfam; PF00048; IL8; 1.  
DR PRINTS; PR00436; INTERLEUKIN8.  
DR PRINTS; PR00437; SMALLCYTCKXC.  
DR PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.  
KW Cytokine; Chemotaxis; Inflammatory response; Signal; 3D-structure.  
FT SIGNAL 1 27  
FT CHAIN 28 100 MACROPHAGE INFLAMMATORY PROTEIN 2.  
FT DISULFID 36 62  
FT DISULFID 38 78  
FT SEQUENCE 100 AA; 10621 MW; B9EF0A3218EE92B5 CRC64;  
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Query Match 68.9%; Score 261; DB 1; Length 100;  
Best Local Similarity 65.8%; Pred. No. 5.5e-23;  
Matches 48; Conservative 12; Mismatches 13; Indels 0; Gaps 0;  
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QY 1 APLATELRQCLOTFLOGIHLKNTOSVKVKGSPGHCAOTEVIATLKNGOKACLNPSPMVK 60  
| : |||||::|| | : ||||| : |||||::||| || |||::|||:  
Db 28 AVVASELRCOCLTLPRVDENQLSQSLVTPPGPHCAOTEVIATLKGGQKVCILDPEAPLVQ 87  
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QY 61 KIIEKMLKNKSN 73  
| ||::|| ||::||  
Db 88 KIIQILNKKGN 100  
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RESULT 14  
GRO_CAVPO STANDARD; PRT; 104 AA.  
ID GRO_CAVPO  
AC O55235;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE GROWTH REGULATED PROTEIN PRECURSOR.  
GN SCYB1 OR GRO.  
OS Cavia porcellus (Guinea pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.  
OX NCBI_TaxID=10141;  
[1]  
RN SEQUENCE FROM N.A.  
RP STRAIN=STRAIN 2;  
RC Yoshimura T., Modi W.S.;  
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
[2]  
RN SEQUENCE FROM N.A.  
RP STRAIN=HARTLEY WHITE; TISSUE=Spleen;  
RC Yoshimura T., Takeya M., Ogata H., Gillitzer R.;  
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: HAS CHEMOTACTIC ACTIVITY FOR NEUTROPHILS.  
CC -!- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE  
CC C-X-C) (CHEMOKINE CXC).  
-----  
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CC EMBL; U95809; AAB93925.1; -.  
DR DR
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DR EMBL; U95810; AAB93926.1; -.
DR EMBL; AF052004; AAC06227.1; -.
DR EMBL; AF052005; AAC06228.1; -.
DR InterPro; IPR001089; -.
DR InterPro; IPR001811; -.
DR InterPro; IPR002473; -.
DR Pfam; PF00048; IL8; 1.
DR PRINTS; PR00436; INTERLEUKIN8.
DR PROSITE; PS00437; SMALLCYTOKINE.
KW Cytokine; Growth factor; Inflammatory response; Signal.
FT SIGNAL 1 31
FT CHAIN 32 104
FT DISULFID 40 66
FT DISULFID 42 82
FT DISULFID 42 82
SQ SEQUENCE 104 AA; 11069 MW; DAFD96D9F4041D5A CRC64;

Query Match 67.8%; Score 257; DB 1; Length 104;
Best Local Similarity 61.1%; Pred. No. 1.6e-22;
Matches 44; Conservative 19; Mismatches 9; Indels 0; Gaps 0;

QY 1 APLATELCQCLQTLQGLHNLKNIQSVKPGPHCAQTEVIATLNGQKACLNPAWPKV 60
DB 32 APAASELCRCRLRPVRLHPLKNIQSVAVTAPGPHCHQTEVLATLKDGREACLDPEAPMVQ 91

QY 61 KIEKMLKNGKS 72
DB 92 KVLQRLKNGSKA 103

RESULT 15
MIP2_RAT STANDARD; PRT; 100 AA.
AC P30348;
DT 01-APR-1993 (Rel. 25, Last Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE MACROPHAGE INFLAMMATORY PROTEIN 2 PRECURSOR (MIP2) (CINC-3).
GN SCYB2 OR MIP2 OR MIP-2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Driscoll K.;
RL Submitted (APR-1992) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=FISCHER;
RL TISSUE=Lung;
RN [3]
RP SEQUENCE FROM N.A.
RA Feng L., Xia Y., Yoshimura T., Wilson C.B.;
RL "Modulation of neutrophil influx in glomerulonephritis in the rat
with anti-macrophage inflammatory protein-2 (MIP-2) antibody.";
RN [4]
RP SEQUENCE FROM N.A.
RA Farone A., Farone M., Shi M.M., Kobzik L., Paulauskis J.D.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 39-91 FROM N.A.
RA MEDLINE=93035653; PubMed=1415488;
RL "Expression of macrophage inflammatory protein-2 and KC mRNA in
pulmonary inflammation.";
RN [6]
RP SEQUENCE OF 32-100.
RA STRAIN=WISTAR;
```

```
RX MEDLINE=94318061; PubMed=8043001;
RA Nakagawa H., Komorita N., Shibata F., Ikesue A., Konishi K.,
RA Fujioaka M., Kato H.;
RT "Identification of cytokine-induced neutrophil chemoattractants
(CINC), rat GRO/CINC-2 alpha and CINC-2 beta, produced by granulation
tissue in culture: purification, complete amino acid sequences and
characterization.";
RL Biochem. J. 301:545-550(1994).
RN [6]
RP SEQUENCE OF 32-59.
RC STRAIN=WISTAR;
RX MEDLINE=96183056; PubMed=8607872;
RA Nakagawa H., Shiota S., Takano K., Shibata F., Kato H.;
RT "Cytokine-induced neutrophil chemoattractant (CINC)-2 alpha, a novel
member of rat GRO/CINCs, is a predominant chemokine produced by
lipopolysaccharide-stimulated rat macrophages in culture.";
RL Biochem. Biophys. Res. Commun. 220:945-948(1996).
CC -!- FUNCTION: CHEMOTACTIC FOR HUMAN POLYMORPHONUCLEAR LEUKOCYTES BUT
CC DOES NOT INDUCE CHEMOKINESIS OR AN OXIDATIVE BURST. CONTRIBUTES TO
CC NEUTROPHIL ACTIVATION DURING INFLAMMATION.
CC -!- SUBUNIT: HOMOTETRAMER.
CC -!- TISSUE SPECIFICITY: AT LEAST EXPRESSED IN THE LUNG AND TRACHEA.
CC -!- INDUCTION: IN LUNG, BY LIPOPOLYSACCHARIDE OR INFLAMMATION.
CC -!- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
CC C-X-C) (CHEMOKINE CX-C).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X65647; CAA46599.1; -.
DR EMBL; S77604; AAB33749.1; -.
DR EMBL; U45965; AAA92438.1; -.
DR EMBL; S45855; -. NOT_ANNOTATED_CDS.
DR PIR; S21467; S21467.
DR HSP; P10889; ILM2.
DR InterPro; IPR001089; -.
DR InterPro; IPR001811; -.
DR InterPro; IPR002473; -.
DR Pfam; PF00048; IL8; 1.
DR PRINTS; PR00436; INTERLEUKIN8.
DR PRINTS; PR00437; SMALLCYTOKINE.
DR PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
KW Cytokine; Chemotaxis; Inflammatory response; Signal.
FT SIGNAL 1 31
FT CHAIN 32 100
FT DISULFID 36 62
FT DISULFID 38 78
FT DISULFID 38 78
SQ SEQUENCE 100 AA; 10783 MW; 4299DFE68FF37A9B CRC64;

Query Match 65.7%; Score 249; DB 1; Length 100;
Best Local Similarity 62.0%; Pred. No. 1.3e-21;
Matches 44; Conservative 14; Mismatches 13; Indels 0; Gaps 0;

QY 3 LATELCRCQCLQTLQGLHNLKNIQSVKPGPHCAQTEVIATLNGQKACLNPAWPKV 62
DB 30 VASELCRCQCLTTLPRVDFRNQISLTTPPGPHCAQTEVIATLNGQKACLNPAWPKV 89

QY 63 IEKMLKNGKSN 73
DB 90 VQKILNKGKSN 100

Search completed: May 4, 2001, 07:36:07
Job time: 39 sec
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 4, 2001, 07:35:28 ; Search time 19.46 Seconds
(without alignments)
439.680 Million cell updates/sec

Title: US-09-467-160-3

Perfect score: 379

Sequence: 1 APLATELRQCQLTQLOGIHL.....PASPVMVKIIEKMLKNGKSN 73

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Archived: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL15:
1: sp_archaea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_mhc:
8: sp_organelle:
9: sp_phage:
10: sp_plant:
11: sp_rodent:
12: sp_unclassified:
13: sp_vertebrate:
14: sp_virus:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	300	79.2	108	6 Q28724	Q28724 oryctolagus
2	241	63.6	59	6 Q62764	Q62764 equus caball
3	179.5	47.4	104	13 Q73912	Q73912 gallus gall
4	170.5	45.0	105	11 Q92126	Q92126 mus musculus
5	141.5	37.3	101	6 Q9XSX5	Q9XSX5 felis silve
6	137	36.1	33	11 Q9Q007	Q9Q007 rattus sp.
7	133	35.1	54	4 Q9UC64	Q9UC64 homo sapien
8	129	34.0	48	6 Q9TR91	Q9TR91 bos taurus
9	125.5	33.1	134	14 Q9YV49	Q9YV49 gallid herp
10	125.5	33.1	142	14 Q9IBJ7	Q9IBJ7 turkey herp
11	125.5	33.1	203	14 Q67634	Q67634 gallid herp
12	123	32.5	31	6 Q97800	Q97800 bos taurus
13	117	30.9	101	13 Q93442	Q93442 lampetra fl
14	108	28.5	34	11 Q9QV88	Q9QV88 rattus sp.
15	107	28.2	40	11 Q9QV74	Q9QV74 rattus sp.
16	105.5	27.8	41	6 Q9XSD2	Q9XSD2 oryctolagus
17	90.5	23.9	86	11 Q9QX28	Q9QX28 mus musculus
18	88.5	23.4	99	11 Q9JHH7	Q9JHH7 mus musculus
19	87.5	23.1	111	4 Q9NS21	Q9NS21 homo sapien

ALIGNMENTS

RESULT 1

Q28724	Q28724	PRELIMINARY;	PRT;	108 AA.
ID	Q28724;			
AC	Q28724;			
DT	01-NOV-1996 (TREMBLrel. 01, Created)			
DT	01-AUG-1999 (TREMBLrel. 11, Last sequence update)			
DT	01-OCT-2000 (TREMBLrel. 15, Last annotation update)			
DE	GRO (PERMEABILITY FACTOR 2).			
GN	RPF2.			
OS	Oryctolagus cuniculus (Rabbit).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.			
OX	NCBI_TaxID=9986;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=NEW ZEALAND WHITE;			
RA	Yoshimura T., Modi W.S.;			
RT	"Isolation of novel GRO genes, and a phylogenetic analysis of the CXC			
RT	chemokine subfamily in mammals.";			
RL	Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE OF 43-108 FROM N.A.			
RC	STRAIN=NEW ZEALAND WHITE;			
RA	MEDLINE=95129889; PubMed=7828903;			
RA	Johnson M.C., Goodman R.B. II, Kajikawa O., Wong V.A., Mongovin S.M.,			
RT	Martin T.R.;			
RT	"Cloning of two rabbit GRO homologues and their expression in alveolar			
RT	macrophages.";			
RL	Gene 151:337-338(1994).			
DR	EMBL; U95808; AA933924.1; -			
DR	EMBL; L28933; AAA66975.1; -			
DR	HSSP; P19875; IQNK.			
DR	INTERPRO; IPR001089; -			
DR	INTERPRO; IPR001811; -			
DR	INTERPRO; IPR002473; -			
DR	PFAM; PF00048; IL8; 1.			
DR	PRINTS; PR00436; INTERLEUKIN8.			
DR	PRINTS; PR00437; SMALLCYTKXC.			
DR	PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.			
SQ	SEQUENCE 108 AA; 11261 MW; 9C278041FC7A5BAD CRC64;			

Q9Jhh5 mus musculus
Q9qzd1 rattus norv
Q68406 human cytom
Q9qv82 rattus sp.
Q9j2m1 macaca mula
Q23352 caenorhabdi
Q9ptf8 brachydanio
Q9quh5 rattus sp.
Q32914 mycobacteri
Q90825 gallus gall
Q9wrt7 macaca mula
Q9u5y1 dictyosteli
Q82851 jembrana di
Q9qv73 rattus sp.
Q9ukz1 homo sapien
Q9lqm5 arabidopsis
Q98158 kaposi's sa
Q60645 homo sapien
O81815 arabidopsis
Q96437 eimeria ten
Q9lgt8 oryza sativ
Q9tcs6 bos taurus
Q29443 archaeoglob
Q9x6x2 myxococcus
O92368 vesv-like c

RA	Sick C., Schneider K., Staeheli P., Weining K.C.;
RT	*Novel chicken CXc and CC chemokines.*;
RL	Cytokine 12:181-186(2000).
RN	[3]
RP	SEQUENCE FROM N.A.
RA	Hughes S.M., Bumstead N.;
RT	*Mapping of a second ELR CXc chemokine to chicken chromosome four.*;
RL	Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR	EMBL; Y14971; CAA75212.1; -.
DR	ENBL; AF277660; AAF86485.1; -.
DR	HSSP; P02775; ITVX.
DR	INTERPRO; IPR001089; -.
DR	INTERPRO; IPR001811; -.
DR	PFAM; PF00048; IL8; 1.
DR	PRINTS; PR00437; SMALLCYTKCX.
DR	PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
KW	Signal.
FT	SIGNAL
FT	CHAIN
SQ	SEQUENCE 104 AA; 11199 MW; 83725AB91FE18E3D CRC64;
Query Match	47.4%; Score 179.5; DB 13; Length 104;
Best Local Similarity	50.7%; Pred. No. 1.4e-13;
Matches 36; Conservative	13; Mismatches 21; Indels 1; Gaps 1;
QY	4 ATEURCCLOCT-LQGIIHLKNIQSVKSPGPHCAQTVEIATLKNGOKACLNPAASPVKKI 62 : : : : :
Db	29 AIEURCCIEFHSFIHPKFIONVLTPSGPHCKNVETIATLRDGREVCIDPTAPWKLI 88 : : : :
QY	63 IEKLKNGKSN 73 : : :
Db	89 IKAILDKADTN 99 : : :
RESULT 4	
Q9Z126	PRELIMINARY; PRT; 105 AA.
ID Q9Z126	PRELIMINARY; PRT; 105 AA.
AC Q9Z126	
DT 01-MAY-1999	(TrEMBLrel. 10, Created)
DT 01-MAY-1999	(TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2000	(TrEMBLrel. 15, Last annotation update)
DE PLATELET FACTOR 4.	
GN PF4.	
OS Mus musculus (Mouse).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
OX NCBI_TaxID=10090;	
RN RN	SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=SPLEEN;	
RA Watanabe O., Tanari M., Natori K., Kubo S., Shiomoto Y., Nakamura Y.;	
RT *Isolation of the murine homologue of rat and human Pplatelet factor	
RL 4cDNA from the spleen of NOA mouse that is a new atopic dermatitis	
RT model by a differential display method.*;	
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.	
DR ENBL; AB017491; BAA75660.1; -.	
DR HSSP; P02776; IRHP.	
DR MGD; MG1:1888711; Pf4.	
DR INTERPRO; IPR001089; -.	
DR INTERPRO; IPR001811; -.	
DR INTERPRO; IPR002473; -.	
DR PFAM; PF00048; IL8; 1.	
DR PRINTS; PR00436; INTERLEUKIN8.	
DR PRINTS; PR00437; SMALLCYTKCX.	
DR PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.	
SQ SEQUENCE 105 AA; 11243 MW; 94F0190EFACF1A6C CRC64;	
Query Match	45.0%; Score 170.5; DB 11; Length 105;
Best Local Similarity	49.2%; Pred. No. 1.6e-12;
Matches 32; Conservative	18; Mismatches 14; Indels 1; Gaps 1;

RESULT	6
Q90Q07	
ID	Q90Q07 PRELIMINARY; PRT; 33 AA.
AC	Q90Q07;
DT	01-MAY-2000 (TReMBLrel. 13, Created)
DT	01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT	01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE	CHEMOATTRACTANT P-3 (FRAGMENT).
OS	Rattus sp.
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX	NCBI_TaxID=10118;
RN	[1]
RP	SEQUENCE.
RX	MEDLINE=93228656; PubMed=8471066;
RA	Komagawa H., Ikesue A., Hatakeyama S., Kato H., Gotoda T.,
RA	Nakamita N., Watanabe K., Miyai H.
RT	"Production of an interleukin-8-like chemokine by cytokine-stimulated
RT	rat NK-49F fibroblasts and its suppression by anti-inflammatory
RT	steroids."
RL	Biochem. Pharmacol. 45:1425-1430(1993).
RD	HSSP; P19875; IQNK.

QY 21 KNIQSVKSPGPHCAQTEVIATLKNQKACLNPA SPVKKIIERMLKN 69
: : | : : | | | : : | | | | : | : : | | : : | : :
Db 6 RHITSLEVIKAGPHCPTAQLIATLKNGRKICLDLQAPLYKKIIKULES 54

RX MEDLINE=95085008; PubMed=7992841;
RA Allmann-Iselin I., Car B.D., Zwahlen R.D., Mueller-Schupbach R.,
RA Wyder-Walther M., Steckholzer U., Walz A.;
RT Bovine ENA, a new monocyte-macrophage derived cytokine of the
RT interleukin-8 family. Structure, function, and expression in acute


```
Db 97 LAVDRCKVKVNRPTGLGPIIAVDVIPGIIHCRTEIIFALKKNRKVCVDPEAPWVQO 156
Qy 62 IIEKM 66
   !:
Db 157 FIKKL 161

RESULT 12
ID O97800 PRELIMINARY; PRT; 31 AA.
AC O97800;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE EPITHELIAL CELL INFLAMMATORY PROTEIN-1 (ECIP-1) (FRAGMENT).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A., AND INDUCTION.
RC TISSUE-KIDNEY EPITHELIAL;
RX MEDLINE=99122841; PubMed=9922392;
RA Heaton M.P., Laegreid W.W., Beattie C.W., Smith T.P.L., Kappes S.M.;
RT "Identification and genetic mapping of bovine chemokine genes
expressed in epithelial cells.";
PL Mamm. Genome 10:128-133(1999).
CC -!- INDUCTION: BY THREEFOLD IN THE PRESENCE OF LPS AND BY FOURFOLD IN
CC THE PRESENCE OF LPS AND CYCLOHEXIMIDE.
CC -!- SIMILARITY: TO GRO-GAMMA AND TO E.CABALLUS MELANOMA GROWTH
CC STIMULATORY ACTIVITY PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
CC C-X-C) (CHEMOKINE CXCL).
DR EMBL; AF061522; AAD02809.1; -.
DR HSSP; P19875; 1QNK.
DR INTERPRO; IPR001811; -.
DR PFAM; PF00048; IL8; 1.
KW Cytokine; Inflammatory response.
FT NON_TER 1
FT NON_TER 31
SQ SEQUENCE 31 AA; 3386 MW; 74172DC13D3A72B8 CRC64;

Query Match 32.5%; Score 123; DB 6; Length 31;
Best Local Similarity 74.2%; Pred. No. 1.5e-07;
Matches 23; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 43 TLKGOKACLNAPSPMVKKIIEKMLKNGKSN 73
   !!!!!!!
Db 1 TLKGQEAELNAPSPMVKKIINKMLKNGSTN 31

RESULT 13
O93442
ID O93442 PRELIMINARY; PRT; 101 AA.
AC O93442;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE LFCA-1 PROTEIN PRECURSOR.
OS Lampetra fluviatilis (River lamprey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
Petromyzontiformes; Petromyzontidae; Lampetra.
OX NCBI_TaxID=7748;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LEUKOCYTES;
RA Najakshin A.M., Mechetina L.V., Alabyev B.Y., Taranin A.V.;
RT "Identification of the interleukin 8 homologue in lamprey (Lampetra
fluviatilis): early evolutionary divergence of chemokines.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ231072; CAAL13114.1; -.
```

```
DR HSSP; P02775; 1TVX.
DR INTERPRO; IPR001089; -.
DR PFAM; PF00048; IL8; 1.
DR PRINTS; PR00437; SMALLCYTKXC.
KW Signal.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 101 LFCA-1 PROTEIN.
SQ SEQUENCE 101 AA; 11095 MW; 80CFEE81EA7336D2 CRC64;

Query Match 30.9%; Score 117; DB 13; Length 101;
Best Local Similarity 34.3%; Pred. No. 2.5e-06;
Matches 23; Conservative 18; Mismatches 24; Indels 2; Gaps 2;

QY 8 RCOCLOTL-OGIHLKNIOQSVKSPGPHCAQTEVIATLKN-GOKACLNAPSPMVKKIIEK 65
   !!!!!!!
Db 30 RCOCVHVISFIHPKHFPQTEVPIQSSNCNKNEIIVTMKSTNNQICLNPDAPWVRKVISH 89
   !:
QY 66 MLKNGKS 72
   !:
Db 90 ILDGAQT 96

RESULT 14
O9QV88 PRELIMINARY; PRT; 34 AA.
ID O9QV88
AC O9QV88;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE MACROPHAGE INFLAMMATORY PROTEIN 2 (FRAGMENT).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE.
RX MEDLINE=93192044; PubMed=8393510;
RA Driscoll K.E., Hassenbein D.G., Carter J., Poynter J., Asquith T.N.,
RA Grant R.A., Whitten J., Purdon M.P., Takigiku R.;
RT "Macrophage inflammatory proteins 1 and 2: expression by rat alveolar
macrophages, fibroblasts, and epithelial cells and in rat lung after
mineral dust exposure.";
RL Am. J. Respir. Cell Mol. Biol. 8:311-318(1993).
DR HSSP; P10889; 1MI2.
DR INTERPRO; IPR001089; -.
DR PFAM; PF00048; IL8; 1.
DR PRINTS; PR00437; SMALLCYTKXC.
SQ SEQUENCE 34 AA; 3762 MW; ECF6DD4262F44782 CRC64;

Query Match 28.5%; Score 108; DB 11; Length 34;
Best Local Similarity 61.8%; Pred. No. 9e-06;
Matches 21; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 5 TELRCOCLOTLQLOGIHLKNIOQSVKSPGPHCAQT 38
   !!!!!!!
Db 1 SELRCOCLKTLPRVDFKNIOQLVTPPGPYXAQT 34

RESULT 15
O9QV74 PRELIMINARY; PRT; 40 AA.
ID O9QV74
AC O9QV74;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE MACROPHAGE INFLAMMATORY PROTEIN 2 HOMOLOG (FRAGMENT).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
```

OX NCBI_TaxID=10118;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=93285151; PubMed=8508797;
 RA Watanabe K., Iida M., Takaishi K., Suzuki T., Hamada Y., Iizuka Y.,
 RA Tsurufuji S.;
 RT "Chemoattractants for neutrophils in lipopolysaccharide-induced
 RT inflammatory exudate from rats are not interleukin-8 counterparts but
 RT gro-gene-product/melanoma-growth-stimulating-activity-related
 RT factors.";
 RL Eur. J. Biochem. 214:267-270(1993).
 DR HSP; P10889; IMI2.
 SQ SEQUENCE 40 AA; 4500 MW; 330DF13BAE51ACFD CRC64;

Query Match 28.2%; Score 107; DB 11; Length 40;
 Best Local Similarity 59.0%; Pred. No. 1.4e-05;
 Matches 23; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 6 ELRCQCLOTIQTGIIHLKNIQSVKVKSPGPHCAQTETVATL 44
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 2 ELRXQXLKTLPRVDFENIQSLTVPPTGPHXTQTETVIAAL 40

Search completed: May 4, 2001, 07:35:55
 Job time: 27 sec